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Result
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1: /SIDS1/gcgdata/hold-geneseq/geneseqp.embl/AA1980.DAT:*

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3: /SIDS1/gcgdata/hold-geneseq/geneseqp.embl/AA1982.DAT:*

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5: /SIDS1/gcgdata/hold-geneseq/geneseqp.embl/AA1985.DAT:*

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10: /SIDS1/gcgdata/hold-geneseq/geneseqp.embl/AA1989.DAT:*

11: /SIDS1/gcgdata/hold-geneseq/geneseqp.embl/AA1999.DAT:*

12: /SIDS1/gcgdata/hold-geneseq/geneseqp.embl/AA1991.DAT:*

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Match
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  99.0
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Copyright (c) 1993 - 2000 Compugen Ltd.
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               Cancer metastasis
Gene encoding the
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Streptcocccus pneu
Streptcocccus faeca
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Mycoplasma hyopneu
43kd regression as
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Novel human diagno	ABG05425	22	674	5.1	110.5	Ů.
Scorpion protein d	AAY70770	21	491	٠	110.5	-
Enterococcus faeca	AAU35313	22	1300		٠	w
Enterococcus faeca	AAU33407	22	1300		111.5	١
Propionibacterium	AAU46975	22	469	•		_
Haemophilus influe	AAB23860	21	2411	5.2	112	_
S. aureus SdrE pro	AAY08643	20	1166	٠	112.5	•
	AAR99393	17	2353		113	ű
Arabidopsis	AAG51608	21	682	٠	113	7
Arabidopsis	AAG51609	21	652		113	٠.
Arabidopsis th	AAG51610	21	646		113	٠.
	AAG82935	22	5024	٠	115.5	-
Mutant C-beta prot	AAW40538	19	1099	5.4	116.5	w
CD.	AAR99392	17	1098	5 5	•	~
Amino acid sequenc	AAG79241	22	719	5.5	117.5	_
lus su	AAW98149	20	2285	5. 5	119	_
	AAY84460	21	1135		119.5	•
Amino acid s	AAY93404	21	834	5.5	119.5	w
Haemophilus	AAB01836	21	1079		121.5	7
Haemophilus	AAB01837	21	1073		121.5	01
Drosophila	ABB63519	22	2346	5.7	122.5	٠.
Amino acid	AAW28236	18	441		130	_
Plasmodium fal	AAB18324	21	1558		131.5	•
P. falcipar	AAW24790	18	1786	6.2	133.5	
M. catarr	AAW68208	19	889		137.5	_
Borrelia	AAE03741	22	353	6.6	143	_
toco	AAY91298	21	223	7.0	151.5	•
-	AAY19984	20	339	7.5	161	ω
•	AAW61757	19	339	7.5	161	~
rferi an	AAY19985	20	322	7.5	161	٠,
•	AAR31013	14	340	7.6	164.5	٠.
	AAR33280	14	341		171	_
>2	AAU07352	22	166	8.0	173	ω
Enterococcus faeca	AAY00048	20	361	8.3	178	.~

## ALIGNMENTS

RESULT AAU01859

AAU01859 standard; Protein;

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11-APR-2001 EP1090995-A2 Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Mycoplasma hyopneumoniae /note= : 174 /note= "Encoded by TGA" 152 /note= "Encoded by TGA" 99 /note= "Encoded by TGA" 138 /note= 246 198 Location/Qualifiers /note= 'note= "Encoded by TGA "Encoded "Encoded "Encoded by TGA by TGA" by TGA"

MHP3; antigen; vaccine; enzootic mycoplasma pneumonia; antibody; immunoassay; immunotherapy; anti-idiotypic antibody.

Mycoplasma hyopneumoniae MHP3 antigen

07-SEP-2001 AAU01859;

(first entry)

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Matches
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  AAU01860;
                         AAU01860 standard;
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                                                                                      NKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSL
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                                                                                                                              ndnsfnqssweaiqqlgaltggeitsvdsstaelegkysslantnknvwvlsgfqhgdaf 149
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Pred. No. 8.6e
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1.6e-163;
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Matches 416;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 19-21; 38pp; English
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                                                                                                                                                                                                                                                                  423 AA;
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                                                                                                                                                                                                           98.4%; Score 2120; DB 22 100.0%; Pred. No. 1e-161;
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                                                                                                                                                       07-MAR-1986;
16-SEP-1987;
11-DEC-1987;
04-JAN-1988;
16-MAR-1990;
02-OCT-1992;
Regression associated antigens (RAA's) are identified in material from neoplastic cells by their immunological reactivity with regression associated antibodies from the serum of patients
                                                      DNA encoding a regression-associated antigen from M. is used to obtain prods. for diagnosis, localisation of tumours % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                          Regression associated antigen; tumour; anti-idiotypic antibodies; antibodies;
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                                   Disclosure; Figure
                                                                                          N-PSDB;
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DB; AAQ47816.
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87US-0097910.
87US-0131815.
88US-0138923.
90US-0474730.
92US-0956546.
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Best Local Similarity
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                                                                                                                                                         Cancer metastasis;
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                        AAP93343;
         01-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ79124 encodes AAR67582 a protein involved in cancer metastasis which may be used for the study of metastaic mechanisms, and for clinical tests to determine the presence or absence of cancer
                                         AAP93343
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                         standard;
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Pred. No. 3.6e-47;
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Mismatches
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Peptide
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Regression-associated antigens may be used in diagnostic tests, eg in vivo imaging, for monitoring the course of therapy or for therapeutic purposes, eg active immunisation protocols in cancer patients or drug delivery systems by binding the drug to monocional or monospecific polyclonal Ab showing specific immunoreactivity with the Ag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour regression-associated antigens used in diagnostic tests, monitoring therapy in cancer patients
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N-PSDB; AAN90684.
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YLGIKDREVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEM-PDK 404
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                                                                                                                                                                                                                        AGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKITT 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 642.5; DB 10;
Pred. No. 3.9e-43;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the inflammatory cytokine of the invention. The inflammatory cytokine can be used in a drug, which useful for the treatment of thrombocytopaenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP11089582-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY05332;
                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New inflammatory cytokine inducer gene and polypeptide - useful for treatment of thrombocytopaenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAX33847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inflammatory
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  307
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425 dakhnekalnelikkin 441
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                                                                                                                                                                                                                                                                    31 NERKSEIMAAKADANKH-------FGLNMAIVTAGGTVNDNSFNQSGWEAI 74
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                        FFTSILKNLGYSVFSVLSDL-----YTKKSNSRNLAGFEFGKKSATVYLGIKDRF
                                                           IAS-----KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVTTDQSLVYTKTKNK 303
                                                                                                                                            ernqikiigidf-dieteykw--fyslqfnikesafttgyaiaswlseq---deskrvva
                                                                                                                                                                                                                  QQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLF 134
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iltsvlkhikqavyetlldlilekeegykpyvvkdkkadkkwshfgtq-----kekw
                                                vinnvlsstpadvkynphvilsvagpat--fetvrlankgqyvigvosdqgmi--qdkdr
                                                                                             sfgggafpgvttfnegfakgilyynqkh--ksskiyhtspvkldsgf-----tagekmnt
                                                                                                                      VIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQ
                                                                                                                                                                       TEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI 194
                                                                                                                                                                                             kainkqtgieinnveps-snfesaynsalsaghkiwvlngfkhqqsikqy--idahreel 143
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                                                                                                                                                                                                                                                                                                                                                                                                                               Page 16-17; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                         428
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26.7%;
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Pred. No. 4.6e-22;
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13 ADNONKQIT----DVSKISGLVNERKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQ

Conservative

Indels

64;

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80 68

SGWEATQQLGALTGGETTSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIP 128 safealkainkqtgieinnveps-snfesaynsalsaghkixvlngfkhqqsikqy--id 137

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 Query Match
Best Local Similarity
Matches 117; Conserv
                                                                   This sequence is a membrane protein designated M161Ag. Oligonucleotide probes for the cDNA were designed from putative N-terminal M161Ag pept sequences isolated from P93 cells. M161Ag can be used in the developme of a leukaemia treating agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW22727 standard; Protein;
                                                 Sequence
                                                                                                                     Claim 1; Fig 1; 6pp; Japanese
                                                                                                                                        Membrane protein M161Ag treating agent
                                                                                                                                                                      WPI; 1997-369470/34.
N-PSDB; AAT75133.
                                                                                                                                                                                                                       05-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Membrane protein
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                                                                                                                                                                                                                                                                                                                                   Modified-site
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348
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185
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         17.3%;
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                                                                                                                                                                                                                                                                                                     "selenocysteine"
                                                                                                                                                   1
                                                                                                                                                   useful
; Score 372; DB 18;
; Pred. No. 1.9e-21;
88; Mismatches 167;
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                    Length 429;
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AAY81501 to AAY81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antiinflammatory properties. The sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be used in vaccines and in diagnostic assays. The nucleotide sequences can be used in vaccines and in diagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection
                                                                                                                                                                                                                                 New Streptococcal protein, useful as a vaccine, pneumococcal diseases and for screening agents or inhibiting expression of the protein -
                                                                                                                                                                                                                                                                                                                                                                                                   27-JUL-1998;
19-MAR-1999;
                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                    WPI; 2000-195300/17.
                                                                                                                                                                                                                                                                                                                                   Gilbert CFG,
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                                                                                                                                                                                                   Page 85; 108pp; English.
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99US-0125164.
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         Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
                                                             WPI; 1998-272224/24.
N-PSDB; AAV27326.
                                                                                                                                                                                                                                                                                                                         Streptococcus
                                                                                                                                                                                                                                                                                                                                                    02-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                     AAW55066 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and meningitis. \mbox{AAA05591} to \mbox{AAA05614} represent primers exemplification of the present invention.
                                                                                                   Choi GH,
                                                                                                                                                     31-OCT-1996;
                                                                                                                                                                              30-OCT-1997;
                                                                                                                                                                                                        07-MAY-1998.
                                                                                                                                                                                                                                 WO9818930-A2
                                                                                                                                                                                                                                                          Streptococcus
                                                                                                                                                                                                                                                                                   detection; pneumonia; otitis media; meningitis.
                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                             AAW55066;
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k----avedakakildgsvkvpekz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLATEAISEAKKEFEEKTKTIPAEE 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stlkqvgttvkdi-----snkaergefpggq---vivyslkdkgvdlavtnlseegk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDK 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --ivyqvaggtgagvfaeakslnesrpenekvwvigvdrdqeaegkytskdgkesnfvlv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       esevisrfeagfkagv----asvdpsikvqvdyag-sfg-daakgktiaaaqyaagad-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qstseadyannlqqaagsynlifgv-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSTLLAVAGPL-TEIFSDIIANQNDR-----YLIGVDTDQSL--VYT----KTKNKFFT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       liddvikdqknv-----asvtfadnesgylagvaaak-----ttktkqvgfvggl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSTAELE-----GKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNII 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGA---LTGGEITSVD 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -SPAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDK
                                                                                                                             HUMAN GENOME SCI INC
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                                                                                                  Hromockyj
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                                                                                                                                                                                                                                                                                                                       pneumoniae SP007 protein
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25.5%;
                                                                                                   Johnson
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                                                                                                                                                                                                                                                                                                                                                                                                     328
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Pred. No. 2.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351
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                                                                                                   Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -gfalnna-----vkdaakehtdlnyv 126
                                                                                                   CA;
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, office media or meningitis. Probes based on the nucleic acid
04-MAY-1998;
                                                                                           Enterococcus
                                                                                                                                                                        Enterococcus
                                                                                                                                                                                                                                     AAY00049;
                                                                                                                                                                                                                                                                   AAY00049 standard;
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                               12-NOV-1998
                                                              WO9850554-A2
                                                                                                                          detection;
                                                                                                                                        Enterococcus faecalis; infection; vaccine;
                                                                                                                                                                                                      20-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  esevisrfeagfkagv----asvdpsikvqvdyag-sfg-daakgktiaaaqyaagad-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGI
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                                                                                                                                                                                                                                                                                                                                              -avedakakildgsvkvp
                                                                                                                          attenuation;
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                                                                                                                                                                     faecalis antigenic polypeptide fragment EF021.
                                                                                                                                                                                                    (first entry)
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98WO-US08959
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                                                                                                                                                                                                                                                                    Protein;
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25.7%;
                                                                                                                         antigenic
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Pred. No. 5.4e-08;
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                                                                                                                                        immune response; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 328;
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AAW61758
ID AAW6
XX
AC AAW6
XX
DT 09-S
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standard;

Protein;

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AAW61758 st; AAW61758; 09-SEP-1998

(first entry)

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RESULT 11
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Best Local Similarity
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06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents an antigenic polypeptide fragment isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
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                                                                                                         256
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                                                                         354 VDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD 403
                                                                                                                                                                                                 262 TLLAVAGPLTEIFSDII----
                                                                                                                                                                                                                                                           203 AVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPS
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                                                                                                                                                                                                                                                                                                                                                      63
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                                                                                                                                                                                                                                                                                                                                                                                                                                              33 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGA---LTGGE----
                                                                                                                                                                                                                                                                                                                                                                                                              vdltdgyl--ndkt----
                                                                                                                                                                                                                                                                                                            GIDWIDTENVIPIGRYINLIYKTEEAGWLAGYANASFLAKKFPSDPIKRSAIVIGGGISP
:|| : || : || : || || || : || : ||
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                                                                                                       ktkdgkednftltstlkgvgtavqdianraledk
                                                                                                                                    KTK-----NKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRF
                                                                                                                                                                                                                              vvidrfqagfekgv-adaakelgkeitvdt------kyaasfadpa
                                                                                                                                                                                                                                                                                         ddqidgkknv----vsatfrdneaaylagvaaa-----
                                                                                                                                                                                                                                                                                                                                                    iqsndaadyttnidqavsskfntifgi...-gyllkda...-issaadanpdtnfvli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0066009.
97US-0044031.
97US-0046655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                           -----keavktakdkvisgdvkvpekpe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 178; DB 20;
Pred. No. 4.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                               ----ANQNDR-YLIGVDTDQSL--VYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140;
                                                                                                                                                                                                                                                                                       --netktnkvgfvggeeg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 339;
                                                                                                    fpggehlvy-glkdgg
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В.

burgdorferi antigenic protein

p39 beta.

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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Sim
atches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAR-1991;
05-MAR-1990;
19-FEB-1993;
01-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                       This represents the Borrelia burgdorferi antigenic protein p39 beta. The antigenic protein p39 alpha is immunoreactive with mammalian Lyme borrelios serum. The Borrelia antigenic proteins p39 alpha and p39 beta are used in vaccines to protect against Lyme disease, as assay reagents to detect specific antibodles in the serum (diagnostic of Lyme disease), and to raise antibodles, either for diagnosis (by detecting the corresponding antigen) or in screening agents for ability to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antigenic - for raising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schwan TG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1995;
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                                                                                                                                                                                                                                                                                                ANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSSTAELEGKYSS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1998-413001/35
                                                                                                                                                AGYLAGIKAWNLKNSDKKTKITTDKIEINLGEDVQDTSTKERLEQIASK--DKPSTLLAV
                                                                                                                                                                                                                                                 --LANTNKN----VWVLSGFQHGDAFTRWLKIPENKQLFTEKNII--ILGIDWTDTENVI 153
                                                                                                                                                                                                                                                                        sskkikismlv---dgvlddksfnssaneallrlkkdfpenieevfs--caisgvyssyv
KTIPAEEVRKTLEIP
                     iknnnv----weggk---vvqmglrdgviglpnan
                                               TKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKT 384
                                                                      aaglagigvieaaknlgdgyyvigadqdqs--ylapkn-fitsviknigdalylitge-y
                                                                                                AGPLTEI-FSDIIANQND-RYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLY
                                                                                                                      ygyesgakyan-kdieilseysnsfsdvdig-----rtiaskmyskgidvihf
                                                                                                                                                                        a-----igfiggmkgnivdafr
                                                                                                                                                                                     PTGRYINLTYKTEEAGWLAGY--ANASFLAKKFPSDPTKRSAIVIG--GGISPAVTD-FI 208
                                                                                                                                                                                                                         sdldnlkrngsdliw-lvgymltda--sllvssenpki--sygiidpiygddvqipenli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 borreliosis;
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV35685,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               burgdorferi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Columns
                                                                                                                                                                                                                                                                                                                                                                                        341
                                                                                                                                                                                                                                                                                                                                                                                                               of the proteins.
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simpson WJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins from antibodies or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91US-0664731.
90US-0487716.
93US-0020245.
95US-0396957.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEALTH & HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lyme
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                                                                                                                                                                                                                                                                                                                                     8.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antigenic protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33pp;
                                                                                                                                                                                                                                                                                                                           58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borrelia burgdorferi useful for diagnostic detection of
                                                                                                                                                                                                                                                                                                                         Score 178; DB 19;
Pred. No. 4.8e-06;
8; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SERVICES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p39
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                                                                                                                                                                                                                                                                                                                                                 Length
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illity to inhibit
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RESULT 1
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Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a protein isolated from Enterococcus faecalls. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalls. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalls protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Page 100; 301pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bailey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-NOV-1997;
06-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-NOV-1998.
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                                                                               135
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AVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPS
                                                                                                                                                                                                                                                                                                                                     RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGA---LTGGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1999-070095/06
                                                                                                    ddqidgkknv-----vsatfrdneaaylagvaaa-----netktnkvgfvggeeg
                                                                                                                                                                                                                                                                                ktaesgggkgda----ahsaviitdtggvddksfnqssweglqawgkehdlpegskgyay
                                                                                                                                                                            iqsndaadyttnidqavsskfntifgi----gyllkda-----issaadanpdtnfvli 134
                                                                                                                                                                                                                              ITSVDSS--TAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIIL 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           attenuation;
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      faecalis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     faecalis protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           faecalis
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97US-0044031.
97US-0046655.
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                                                                                                                                                                                                                                                                                                                                                                                                             8.3%;
25.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection;
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                                                                                                                                                                                                                                                                                                                                                                                     51;
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                                                                                                                                                                                                                                                                                                                                                                                     Score 178; DB 20;
Pred. No. 5.3e-06;
1; Mismatches 140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 361;
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                                                                                                                                                                                                                                                                                                                                                                                        116;
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RESULT 1
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                      interleukin-X (IL-X), from an Epstein Barr virus (EBY)-carrying probablastoid cell line. IL-X proteins can be used to enhance the growth of cells in vitro, or to grow primary human be litures to facilitate proliferation of these cell lines, as therapeutics or prophylactics, as molecular weight standards, as inert proteins in an assay, or in the detection of antibodies that are immunoreactive with IL-X. Nucleotide sequences encoding the peptides could be used to produce recombinant peptides or they could be used as probes or primers for diagnostic and/or analytical polymerase chain reaction (PCR) procedures, or as DNA or RNA sizing standards. The present sequence represents the amino acid
                                                                                                                                                          The invention relates to a novel secreted autostimulatory factor, interleukin-X (IL-X), from an Epstein Barr virus (EBV)-carrying
                                                                                                                                                                                                                                    New IL-x polypeptides useful e.g. for enhancing the growth of cells vitro, for growing primary human B cell cultures to facilitate proliferation of these cell lines, as therapeutics or prophylactics, molecular weight standards -
                                                                                                                                                                                                                                                                                                                                                              Blazar BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JAN-2002
           sequence of IL-X.
                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                        08-AUG-1994;
11-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interleukin-X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU07352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU07352 standard; Protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                                                                            (BLAZ/) BLAZAR B A.
(WEBB/) WEBB A C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interleukin-X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lymphoblastoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327
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DB; AAS11798.
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                                                                                                                                                                                                        Page 7; 16pp;
                                                                                                                                                                                                                                                                                                                                                               Webb AC
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93US-0026132
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   B cell.
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                                                                                                                                                                                                                                                    prophylactics,
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           The sequences given in AAR31013 and AAR33280 represent the B. burgdorferi proteins P39-alpha and P39-beta. The DNA encoding these proteins was isolated by polymerase chain reaction (PCR) using the primer sequences given in AAQ34673-76. This DNA contained two open reading frames (ORF). It was therefore concluded that the P39 antigen which has been previously described is not one protein but two, 39-alpha and 39-beta. The P39 signal appears be enhanced when both genes are present. Gene 1 encodes a 339 amino acid protein with a calculated molecular weight of 36.926 kb. The protein encoded by this gene which is reactive with serum from human Lyme patients. The ORF
                                                                                                                                                                                     New Borrelia burgdorferi protein and DNA isolates -detection of Lyme borreliosis infection and in production and vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymerase chain reaction; PCR; primer; open reading frame; antigen; 39-alpha; 39-beta; serum; human; Lyme patient; p39-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
of gene
                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                        WPI; 1993-017799/02.
                                                                                                                                                                                                                                                                                                                                         05-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                    05-MAR-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borrelia burgdorferi.
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11-MAY-1993
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                                                                                                                                                                                                                                                                                    TG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166
                                                                                                                                                             Page 36-39;
                                                                                                                                                                                                                                                                                    Simpson
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  designated p39-beta.
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27.3%;
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Pred. No. 4.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rum; human; Lyme patient;
ribosomal binding site;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -YTKKSNSRNLAGFEFGKKSATVYLGIKDRFVD
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleotides downstream of p39-alpha and encodes a protein of 341 amino acids (37.506 kD). The promoter located 5′ of p39-alpha appears to be present with classic -10 and -35 regions whereas p39-beta lacks a recognisable promoter sequence. Both genes have putative ribosomal binding sites immediatly 5′ to the start codons and each is terminated with a TAA codon. Comparing the genes sequences of p39-alpha and p39-beta indicates that these genes have 62% similarity. (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.)
                 05-MAR-1990;
                                                 05-MAR-1990;
                                                                                                               USN7664731-N
                                                                                                                                                                              Polymerase chain reaction; PCR; primer; open reading frame; ORF; P39, antigen; 39-alpha; 39-beta; serum; human; Lyme patient; p39-beta; p39-alpha; promoter; -10; -35; ribosomal binding site; RBS.
                                                                                01-DEC-1992
                                                                                                                                              Borrelia burgdorferi
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11-MAY-1993
                                                                                                                                                                                                                                                                                                                                 AAR31013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aglagigvieaaknlgdgyyvigadqdqs--ylapkn-fitsviknigdalylitge-y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTIPAEEVRKTLEIP 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a-----yvfrveggaflagyidakksfsgk------igfirgmkgnivdafr 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sskkikismlv---dgvlddksfnssaneallrlkkdfpenieevfs--caisgvyssyv 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lknnnv----weggk---vvqmglrdgviglpnan---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGPLTEI-FSDIIANQND-RYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLY 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTGRYINLTYKTEEAGWLAGYANA--SFLAKKFPSDPTKRSAIVIG--GGISPAVTD-FI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sdldnlkrngsdliw-lvgymltda--sllvssenpki--sygiidpiygddvqipenli 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 AA;
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                 90US-0487716
                                               90US-0487716.
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Pred. No. 1.8e-05;
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                                                                                                                                                                            c; p39-beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92;
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Query Match 7.6%; Best Local Similarity 22.7%; Matches 85; Conservative ( 406 286 239 286 189 232 143 173 114 93 37 PDKQQESLDKLITD YLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDKQ 405 LIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATV 345 DKI----EINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANQ--NDRY GYANASFLAKKFPSDPTKRSAIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITT 231 GFQHGD-AFTRWLKIPENKQLFTEKNIIILGIDWIDTENVIPTGRYINLTYKTEEAGWLA 172 gtfddksfnesalngvkkvkeefkielvlkesssnsylsdleg----lkdagsdliwlig 92 GTVNDNSFNQSGWEAIQQLGALTGGEITSVDSST----AELEGKYSSLANTNKN-VWVLS 113 nyglkegvvgfv-iigvdedqayl---apdnvitsttkdvgral----nift--snhlktntfeggk---li qyigsfadleagrsvatrmysdeid-----iihhaaglggigalevakelgsghy gyiaakl-----sktgkigflggiegeivdafrygyeagakyan----kdikist fyrfsdvakvaalqnpdmkyai-----idpiysndpip-anlvgmtfraeegaflt 142 69; Score 164.5; DB 1 Pred. No. 5.8e-05; 69; Mismatches 135 DB 14; 135; Indels Length 340; 85; Gaps 285 238 285 188 326 19;

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Search completed: July 18, 2002, 15:32:20 Job time: 187 sec

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Title:
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1 MWDKETTKEEKSADNQNKQI......KQPDKQQESLDKLITDINNL 423
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Gapop 10.0 , Gapext 0.5
                                                                                            283138 seqs, 96089334 residues
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Database PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* pir1:\*
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. score grea and is der No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

#### SUMMARIES

Result

		<b>P</b>				
Result No.	Score	7	Length	₽B		<b>-</b>
1	552	25.6	461	ນ	в90555	ABC transporter xy
2			350	Ŋ	F86804	ic membrane p
ω	202		350	N	G95097	
4	198	9.2	374	Ŋ	C97965	conserved hypothet
σı	192	8.9	357	N	D96986	
6	181	8.4	353	1	H71340	
7	180.5	8.4	350	_	C70009	
8	178.5		359	N	F72418	basic membrane pro
	177	8.2	341	N	E70147	basic membrane lip
	173	8	357	N	AH1610	ţ
	168.5	7	516	Ŋ	C82946	hypothetical prote
	168	7	357	N	AD1248	CD4+ T cell-stimul
	165.5	7	360	N	H70147	basic membrane pro
	162.5	7	525	N	C82914	conserved hypothet
15	161	7.5	339	N	F70147	basic membrane pro
16	152.5	7.1	591	N	D64204	membrane lipoprote
17	150		524	Ŋ	D82944	hypothetical membr
18	146	6.8	353	N	G70147	basic membrane pro
19	140	6.5	379	N	H75318	membrane lipoprote
20	139.5	6.5	337	N	B97374	Deinococcus radiod
21	139.5	6.5	337	N	AH2591	membrane lipoprote
22	136	6.3	547	2	E29504	mercury(II) reduct
23	134	6.2	539	N	D82886	conserved hypothet
24	132	6	326	N	G95857	hypothetical prote
25	131.5	6	1558	N	B71603	RESA-H3 antigen PF
26	128	5	657	N	S73428	probable lipoprote
27	126	5	349	N	F84246	hypothetical prote
28	125.5	ر ت	763	N	A82863	
29	125.5	5.8	1223	Ν	E88451	

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probable xylanase/	exported protein (	conserved hypothet	hypothetical prote	hypothetical prote	probable lipoprote	probable type I si	IgA-specific metal	hypothetical prote	peptide ABC transp	probable transglyc	hypothetical prote	lipoprotein [impor	Tpr homolog - frui	ABC transporter (1	colicin Ia - Esche

#### ALIGNMENTS

RESULT B90555

**ب** 

ABC transporter xylose-binding lipoprotein [imported] - Mycoplasma pulmonis (strain U C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 03-Aug-2001
C;Accession: B9055
R;Chambaud, I:; Hellig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma p A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: B90555
A;Status: preliminary
A;Accession: Draininary
A;Mostatus: preliminary
A;Mostatus: preliminary
A;Mostatus: preliminary
A;Mostatus: preliminary
A;Mostatus: 1-461 <KUR>
A;Cross-references: GB:AL445566; PID:g14089760; PIDN:CAC13519.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP C;Genetics: A;Gene: MYPU\_3460 A;Genetic code: SGC3

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33	282 322	225 263	167 203	108 143	62 83	13 28	Query Match Best Local Matches 13
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334 AGFEFGKKSATVYLGIKDREVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEE 391 	NDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNL 333   :::        :  :     :  :         :   :	KKTKITTDKIBINLGFDVQDTSTKERLBQIASKDKPSTLLAVAGPLTEIFSDIIANQ 281       :: ::    ::   	EAGWLAGYANASFLAKKFPSDPTKRSATVIGGGISPAVTDFIAGYLAGIKAWNLKNSD 224          :     :::   :         : :  :    : :: EAGWQAGYASADFLGTKYANNEAKRAISAFGGGDFAGVTDFLNGFFEGIRAWNSEAENAN 262	NVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTEN-VIPTGRYINLTYKTE 166  : :     :     :     :	NDNSFNQSGWEAIQQLGALTGGEITSVDSSTAELEGKYSSLANTNK 107 :	ADNQNKOITDVSKISGLVNERKSBIMAAKADANKHFGLNMAIVTAGGTV 61	Query Match 25.6%; Score 552; DB 2; Length 461; Best Local Similarity 31.2%; Pred. No. 5.1e-27; Matches 133; Conservative 82; Mismatches 161; Indels 50; Gaps 11;

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C;Species: Streptococus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: G95097
C;Accession: G95097
R;Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heimon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: G95097
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A;Cross-references: GB:AE005176; PID:g12724428; A;Experimental source: strain IL1403
C;Genetics:
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C;Geneti
A;Gene:
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J. Bacteriol. 183, 5709-5717, 2001
J. Bacteriol. 183, 5709-5718, 2001
J. Blaszczak, L.; Burgett, S.; D.
J. Blaszczak, L.; Burgett, J.; Burgett, 
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-350 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK74976.1; PID:gl4972319; GSPDB:GN00164; TIGR:
A;Experimental source: strain TIGR4
C;Genetics:
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A; Residues: 1-374 < KUR>
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C;Accession: C97965
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                                      RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGA---LTGGEITSVD
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RSSRNAASSSDVK----TKAAIVTDTGGVDDKSFDQSAWEGLQAWGKEHNLSKDNGFTYF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STLKQVGTTVKDI--
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                                                                                                                                                     97;
                                                                                                                                                                                    Similarity
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                                                                                                                                                 54;
                                                                                                                                                                                Score 198; DB 2;
Pred. No. 4.6e-05;
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Pred. No. 2.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 145;
                                                                                                                                                 Mismatches
                                                                                                                                                 147;
                                                                                                                                                                                                                   Length 374;
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90

GKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNII 140

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probable lipoprotein, Med/BMP family [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: D96986 R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.; Daly, M.J; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Accession: D96986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE001437; PIDN:AAK78679.1; A;Experimental source: Clostridium acetobutylicum C;Genetics: A;Genee: CAC0702
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A;Molecule type: DNA
A;Residues: 1-357 <KUR>
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                                                                                                                                                                                                            TKRSAI-VIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTST
                                                                                                                                                                                                                                                                         DDAYDKQPKNI-
                                                                                                                                                                                                                                                                                                                                                             AKEYSVDYKAIESKKKDDYOPNLOSLIDNDSDLVFGVGYQMADDLATIAKKYPDKKFAII 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTTVMIVAGLEAGCSSTSSGSGNSKDTKK---VKVGLSTDEGGLNDKSFNQGADEGIKKA
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  VILTSMVKRVDIATYNTVKDLVKGKK-----
                                            KFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLG:(KDRFVDIADTSLE 362
                                                                                                                                                                                                                                                                                                                   E-----KNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDP
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                                                                                           GKEVATSLYNGGCDIVYHAAGGAGIGVF-DVAKSLRDQGKDVWAIGVDKDQAAGLPKYAD
                                                                                                                                   -KERLEQIASKDKPSTLLAVAGPLTEIFSDIIANQNDR----YLIGVDTDQSLVYTKTKN 302
                                                                                                                                                                                  TKTNKIGFVGGKDQPLINKFLSGYIAGAKTVN----PNITVEK---NYTNDYSDTSK
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  FEGGKVES - - - FGLKEDGVGVAPTS - -
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A.Gene: tmpC; TP0319
A.Start codon: GTG
C.Superfamily: ABC transporter yufN
C.Superfamily: ABC transporter yufN
C.Keywords: blocked amino end; lipoprotein; membrane protein; thiolester bor F;1-20/Domain: signal sequence #status predicted <SIG>F;1-250/Domain: signal sequence #status tmpC #status predicted <MAT>F;21-353/Product: membrane lipoprotein tmpC #status predicted <MAT>F;21/Modified site: fatty acylated amino end (Cys) (in mature form) #status F;21/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-10,'A',12-158,'R',160-353 <SCH>
A;Residues: GB:X57836; NID:948838; PIDN:CAA40968.1;
A;Note: this protein is shown to incorporate palmitic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Schouls, L.M.; van der Heide, H.G.J.; van Eml
Infect. Immun. 59, 3536-3546, 1991
A;Title: Characterization of the 35-kilodalton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Complete genome sequence of Treponema pallidum, A;Reference number: A71250; MUID:98332770 A;Accession: H71340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane lipoprotein TmpC precursor - syphilis spirochete C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Date: 07-Aug-1998 #sequence_revision 07-Aug-1998 #text_change 23-Jul-1999 C;Accession: H71340; A43595; S29561
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A; Accession: A43595
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Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
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                                                                                                                                                             ANQNDRYLIGVDTDQSL--VYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGF
                                                                                                                                                                                                                                                                                                                                                               LAGYANASFLAKKFPSDPTKRSAI--VIGG--GISPAVTDFIAGYLAGIKAWNLKNSDKK 226
                                                                                                                                                                                                                                                                                                                                                                                                          VACGSFLVEA-----VIETSARFPKQKFLVIDAVVQDRDNV-----VSAVFGQNEGSF 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSST-AELEGKYSSLANTNKNVW
  EIP
                                                                                                                                                                                                                                                                      TKITTDKIEINLGFDVQDT-STKERLEQIASK---DKPSTLLAVAG----PLTEIFSDII
                                                                                                                                                                                                                                                                                                                   LVGVA-AALKAKE-----AGKSAVGFIVGMELGMMPL---FEAGFEAGVKAVD-----
                                                                                                                                                                                                                            -----PDIQVVVEVANTFSDPQKGQALAAKLYDSGVNVIFQVAGGTGNGVIKEARDRR
                                            -----GQSIMFGLEDKAVGIPE-----
                                                                                         EFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.4%; Score 181; DB 1;
23.7%; Pred. No. 0.00049;
htive 69; Mismatches 134
                                            -ENPNLSSAVMEKIRSFEEKI---
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A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler lech, J.; Harwood, C.R.; Hennut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle ger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, thors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serora Keuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchlyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Reference number: A69580; MUID:98044033
A; Accession: C70009
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C;Accessi
basic membrane protein C; Species: Thermotoga r
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A; Residues: 1-350 <KUN>
A; Cross-references: GB:Z99120; GB:AL009126;
A; Experimental source: strain 168
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Best Local
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                                                                                                                                                                                                                                            -KAVDKWKKKIIDGLEIPATEKELKTFKAE
                                                                                                                                                                                                                                                                                                                                                                                                    K----KVDTVVEDV-TKKASDGKFPGGE-----TLTYGLDQDGVGISPSKQNLSDDVI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UDVIYHSAGATGTGVFTB-AKNLKKEDPKRDVWVIGVDKDQYAEGQVEGTDDNVTLTSMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDT--STKERLEQIASKDK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELIKKFEVGFRAGVQAVNPK-----AVVEVKYAGGFDKADVGKATAESM----YKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLA 369
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Pred. No. 0.00052;
0; Mismatches 144;
                                            maritima
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                                            (strain MSB8)
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.M.; Cho
ari, E.
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Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943
A;Accession: E70147

A;Cross-references: GB:AE001143; GB:AE000783; A;Experimental source: strain B31

A; Molecule type: DNA A; Residues: 1-341 <KLE>

A; Status: preliminary; nucleic acid sequence

not shown;

translation

not shown

Borrelia

burgdorferi

on, M.; Hatch,

8 선 돛

NID:g2688279;

PIDN: AAC66758.1;

R;Simpson, W.J.;

Cieplak,

Σ

basic membrane lipoprotein B (bmpB) - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 29-Sep-1999
C;Accession: E70147; I40290; I40242
C;Accession: E70147; I40290; I40242
M.M.; Sutton, G.G.; Clayton, R.; Lathigra,
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, J.; Salzberg, S.; Hanson,
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson,
Son, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hat

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A;Reference number: A72200; MUID:99287316
A;Accession: F72418
A;Status: preliminary
A;Molecular from
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C; Superfamily:
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;Accession: F72418
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Best Local
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                                                                        DVASYYGVVWAYE-
                                                                                                                                                                                                                                                                                                                           NVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGIS-PAVTDFIA 209
                                                                                                                                                                                                                                                                                       QILP--NVLTFTFKEQEAAFLVGYVAAAM-----TKTGMVGFVGGIPIPPVERFRY 161
                   | ISE---AKKEFEEKTKTIP-AEEVRKTLEIPEM 401
                                                                                                      GYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEA 372
                                                                                                                                                                            -- ASKDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNL 312
                                                                                                                                                                                                                 GYEAGIKTYSVLHK-KNVKILRGYTQDFEDPKKGKDLAMSQFAEGADIVFHASGACGNGV
                                                                                                                                                                                                                                                   GYLAGIKAWNLKNSDKKTKI----TTDKIEINLGFDVQDTSTKERLEQI-------
                                                                                                                                                                                                                                                                                                                                                                                                 TAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTE- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDS-S 91
IAELLYLEKLMKEGTLKVPETQEELDAFEVPQI 355
                                                                                                                                          IEAAREKFSA-LAGSDKLVDLIDYYTTNGKGFFAIGVDMDQDYM---APGAVLTSAMKRV
                                                                                                                                                                                                                                                                                                                                                               QSDYIPNLSKAAEEADLVFAVGFMMTNDLFKVAKQYPDT-----YFVGIDITPPEG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                      RKFLVISLMIFAVALFGFKVIMVTDVGGLGDKSFNDGTWAGIKQAAEELGIEAKVIQSYE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clayton, R.A.; Gill, S.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transporter yufN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.3%;
                                                                    -GTFEGGHR----VLGISEDAVGI--SPMKYTKGLVPNRV 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB:AE000512; NID:g4980582; PIDN:AAD35196.1; PID:g498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 178.5; DB 2;
Pred. No. 0.00071;
9; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gwinn, M.L.; Dodson, R..
; Pratt, M.S.; Phillips,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.J.; Haft,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                          276
                                                                                                                                                                                                                                                   254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
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Science 294, 849-852, 2001
A.Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. A.; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AH1610
A; Accession: preliminary
A; Molecule type: DNA
A; Residues: 1-357 < GLA>
A; Residues: 1-357 < GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Nucloetide sequence and analysis of the gene in Borrelia burg A;Reference number: I40289; MUID:94327086
A;Recession: I40290
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross references: GB:L24194; NID:9508420; PIDN:AAA72407.1; PID:g5084
A;Cross references: GB:L24194; NID:9508420; PIDN:AAA72407.1; PID:g5084
R;Ojaimi, C.; Davidson, B.E.; Saint Girons, I.; Old, I.G.
Microbiology 140, 2931-2940, 1994
A;Tritle: Conservation of gene arrangement and an unusual organization
A;Reference number: I40241; MUID:95111614
A;Accession: I40241; MUID:95111614
                                                                                                                                                                                                                                                                     CD4+ T cell-stimulating antigen, lipoprotein [imported] · Listeria innocua (strain C;Species: Listeria innocua (c;Species: Listeria innocua (c;Species: Listeria innocua (c;Species: 17-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AH1610 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blo;; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsih
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A;Cross-references: GB:AL592022; PIDN:CAC96656.1; A;Experimental source: strain Clip11262 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
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                                                                                                                                                                                                                                                      D.; Jones, L.M.; Karst, U
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 ANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSSTAELEGKYSS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --LANTNKN----VWVLSGFQHGDAFTRWLKIPENKQLFTEKNII--ILGIDWTDTENVI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSKKIKISMLV---DGVLDDKSFNSSANEALLRLKKDFPENIEEVFS--CAISGVYSSYV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTGRYINLTYKTEEAGWLAGY - - ANASFLAKKEPSDPTKRSAIVIG - - GGISPAVTD - FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKNNNV-----WEGGK----VVQMGLRDGVIGLPNAN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASK--DKPSTLLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A-----VVFRVEQGAFLAGYIAAKKSFSGK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDLDNLKRNGSDLIW-LVGYMLTDA--SLLVSSENPKI--SYGIIDPIYGDDVQIPENLI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTIPAEEVRKTLEIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATIAISEAKKEFEEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGPLTEI-FSDIIANQND-RYLIGYDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YGYESGAKYAN-KDIEIISEYSNSFSDVDIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGLAGIGVIETAKNLGDGYYVIGADQDQS--YLAPKN-FITSVIKNIGDALYLITGE-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100;
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26.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NID:g516591; PIDN:AAC41402.1; PID:g551744
protein C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 177; DB 2;
Pred. No. 0.00082;
9; Mismatches 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from GB/EMBL/DDB:
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                                           PID:g16413898; GSPDB:GN00178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -EF-EYI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92;
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A ::
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                                                                                                                                                                                        Maitournam, A.; Mo
Voss, H.; Wehland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324
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                                                                                                                                                                                                                                                                       ; Bloecker
Fsihi, H.
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Matches 101;
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Best Local
                                                                                                                                                                                                                                                                       164
313 IEYGLDKDAVGLSE-----HQDNISKDVLAKVE---EYKQKIVDGD-----IKVPEKP
                                       345 VYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMP
                                                                                                                                                                             206 ANDFAKADKGQQIASSMYSSGVDVIFHAAGGTGNGVFAE-AKNLKKKDPSRAVWVIGVDR
                                                                                                                                                                                                                                                                                                                                                           124 QKPKNQFAIVDDTI------DDRDNVVSIG-----FKDNDGSYLVGVVAGL-----
                                                                                                                                                                                                                                                                                                                                                                                                          127
                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 SGLV-----NERKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                DQ-----SLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAG-FEFGKKSAT
                                                                                                                                                                                                                          --DTSTKERLEQIASKDKPS----TLLAVAGPLTEIFSDIIANQNDR-----YLIGVDT
                                                                                                                                                                                                                                                                       --TTKTNKVGFVGGVKGAVIDRFEAGFTAGVKA-------VNPNAQIDVQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                       KANDMEKGTDGYNYLQSASEADYK-----TNLNTAVRSDYDLIYGIGYKLKDAIEEVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALT----GGEITSVDSSTAELEGKYSSLANTNKNVWVLS------GFQHGDAFTRWLK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGVVLGACGSSSDDKKS-----GDDKSSKDFTVAMVTDTGGVDDRSFNQSAWEGLQKFG
                                                                                    DQWDEGKVTANDGKDYNVTLTSEIKRVDIAV----DDLAT----RTKAGDFPGGTK---
                                                                                                                                                                                                                                                                                                                 SDPTKRSAIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQ-
                                                                                                                                                                                                                                                                                                                                                                                                        - IPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 173; DB 2; Pred. No. 0.0016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357;
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357
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A; Molecule type: DNA A; Residues: 1-516 <GLA> A; Cross-references: GB: AEO02100; CA; Experimental source: serovar 3; hypothetical protein UU012 [imported] - Ureaplasma C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 A; Gene: UU012 A; Genetic code: A;Description: The complete sequence A;Reference number: A82870 A;Accession: C82946 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, submitted to GenBank, February 2000 A; Status: preliminary C; Accession: C82946 Query Match Best Local S Matches 110 157 --RYINLTYKTEEAGWLAGYANASFLAKK---FPSDPTKRSAIVIGG--GISPA-VTDFI Local Similarity hes 110; Conserv 17 48 11 ADRVADVYFKVDEAAFLGGIAAAYMLNSNQAVFGAD----TNKNVWVLSGFQHGDAFTRWLKIPENKQ -- LFTEK -- - NIIIL -- - GIDWTDTENVIPTG FALGTIITVATSCTQKSTLNYSQFYW------TSPTSDDDEGFQTKYKSMAS FGLNMAIVTAGGTVNDNSFNQSG--WEAIQQLGALTGGEITSVDSSTAE-LEGKYSSLAN 104 SGC3 Conservative 7.8%; 25.1%; GB:AF222894; NID:g6898946; PIDN:AAF30417.1; biovar 1 PERLQNALVNDKFDPNLIALILDGVYNNDNKAEFYKG Score 168.5; DB 2; Pred. No. 0.0051; 5; Mismatches 167; of Ureaplasma 20-Aug-2000 #text\_change NKLTWGGYVGINAKNTTNYL urealyticum: urealyticum Length Indels 516; Alternate views 20-Aug-2000 E.Y.; Cassell, Gaps 156 168 112 62 26; GSPDB:GN

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A; Residues: 1-357 <GLA>
A; Cross-references: GB:NC_003210;
A; Experimental source: strain EGD-
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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Sinces, N.; Tierrez, A.; Vazquez-Boland, J. A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; A; Recession: AD1248
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; )
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tches 98
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                  272
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               VTANDGKDYNVTLTSEIKRVDIAV----EDLAT----RAKAGDFPGGTK---IEYGLDK
                                                                                DKGQQIASSMYSSGVDVIFHAAGGTGNGVFAE-AKNLKKKDPSRAVWVIGVDRDQWDEGK
                                                                                                               ERLEQIASKDKPS----TLLAVAGPLTEIFSDIIANQNDR-----YLIGVDTDQ-----
                                                                                                                                                   KVGFVGGVKGTVIDRFEAGFTAGVKA----
                                                                                                                                                                                 ATVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQ----DTSTK
                                                                                                                                                                                                                 AIVDDTI-----DDRDNVVSIG-----FKDNDGSYLVGVVAGL-----TTKTN
                                                                                                                                                                                                                                                LFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRS
                                                                                                                                                                                                                                                                                 GTDGYNYLQSASEADYK-----TNLNTAVRSDYDLIYGIGYKLKDAIEEVSKQKPKNQF 130
                                                                                                                                                                                                                                                                                                       GGEITSVDSSTAELEGKYSSLANTNKNVWVLS------GFQHGDAFTRWLK-IPENKQ
                                                                                                                                                                                                                                                                                                                                                 ILGACGSSSDDKKSSDDKSSKDF--TVAMVTDTGGVDDRSFNQSAWEGLQKFGKANDMEK
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                                                -SLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAG-FEFGKKSATVYLGIKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGFDLGVKWANEKLKDKNIKQEGTQETKKWINVEQVYASESSAGGFQSDSANAKKIIQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGYLAGIKAWNLKNSDKKTK---ITTDKIEINL------GFDVQDTSTKERLEQI
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                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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23.8%;
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Pred. No. 0.
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Voss, H.; W
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Fsihi, H.
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                                                                                            A; Description: The complete A; Reference number: A82870 A; Accession: C82914
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C82914
A; Experimental source: C; Genetics:
             A;Cross-references: GB:AE002123; GB:AF222894; NID:g6899229; PIDN:AAF30635.1; A;Experimental source: serovar 3; blovar 1
                                              A; Molecule type: DNA
A; Residues: 1-525 <GLA>
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A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943
A;Accession: H70147
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A; Residues: 1-360 <KLE>
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Best Local :
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A;Cross-references: GB:AE001144; GB:AE000783; NID:g2688291; A;Experimental source: strain B31 C;Superfamily: basic membrane protein C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               basic membrane protein D (bmpD) homolog - Lyme disease spirochete C;Species: Borrella burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 29-Sep-1999 C;Accession: H70147
                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hat Nature 390, 580-586, 1997
     Indels
                                                        Length
                                                                                                                                                                                                                                                                                         translation
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Gaps
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TEIFSDIIANQ--NDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKS 328
                                                                                                                                                                                                                                                                                                                                               AKYAN-----SNIKVVSQYVGTFGDFGLG-----RSTASNM----YRDGVDIIFAAAG-L 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VACSSSDDGKSEAKTVSLI-VDGAFDDKGFNESSSKAIRKLKADLNINIIEKASTGNSYL 92
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                                                                                                                                                                            SGIGVIEAAKELGPDHYIIGVDQDQSYL---APNNVIVSAVKKVDSLMYSL---
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331
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R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, submitted to GenBank, February 2000 conserved hypothetical membrane lipoprotein UU226 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Decies: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000 C;Accession: C82914 sequence of Ureaplasma urealyticum: Alternate views GSPDB:GN G.H. of.

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A; Molecule type: DNA
A; Residues: 1-339 <RES>
A; Residues: 1-339 <RES>
A; Cross-references: GB:L24194; NID:g508420; PIDN:AAA72406.1;
A; Cross-references: GB:L24194; NID:g508420; PIDN:AAA72406.1;
R; Ojaimi, C.; Davidson, B.E.; Saint Girons, I.; Old, I.G.
Microbiology 140, 2931-2940, 1994
A; Title: Conservation of gene arrangement and an unusual orga
A; Reference number: I40241; MUID:95111614
A; Accession: I40241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             basic membrane protein A (bmpA) - Lyme disease spirochet:

N;Alternate names: antigen P39; membrane lipoprotein A
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 29-Sep-1999
C;Accession: F70147; 140289; 140249
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.;
Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.;
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch,
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A; Authors: Smith, H.O.; Venter, J.C.
A; Authors: Smith, H.O.; Venter, J.C.
A; Authors: Smith, H.O.; Venter, J.C.
A; Authors: Special burgdorferi.

Bécrence number: A70100; MUID:98065943

Accession: F70147

A; Status: preliminary; nucleic acid sequence not shown; "ranslation not shown"
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A; Genetic code:
                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-339 <KLE>
A; Cross-references: GB: AE001143; GB: AE000783;
                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                             A; Accession: I40289
                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
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Matches 95
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A; Cross references: GB:L3
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                                                                      347
                                                                                                                                             287
                                                                                                                                                                                                                                                      143 YIAAKL-----SKTGKIGFLGGIEGEIVDAFRYGYEAGAKYAN-----KDIKISTQ
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                                                                                                                                                                               189 YIGSFADLEAGRSVATRMYSDEID------IIHHAAGLGGIGAIEVAKELGSGHYI 238
                                                                                                                                                                                                                                                                                       174 YANASFLAKKFPSDPTKRSAIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITTD
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 DKQQESLDKLITD
                                                                        LGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDKQP
                                     YGLKEGVVGFV----RNPKMISF----
                                                                                                          IGVDEDQAYL---APDNVITSTIKDVGRAL----NIFT--SNHLKINTFEGGK---LIN 285
                                                                                                                                          IGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVY 346
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Search completed: Job time: 43 sec July 18, 2002, 15:29:56

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1 MWDKETTKEEKSADN
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TCSA_LISIN
BMPB_BORGA
TCSA_LISMO
BMPA_BORBU
MCGC_TEVA
WCGD
WCCD_MCCP
Y040_MYCPN
Y040_MYCPN
YA47_SCHPO
XCPC_XENIA
YA67_SCHPO
XCPC_XENIA
PARC_BORBU
TA47_SCHPO
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   Description
 5 mycoplasma
8 mycoplasma
9 schizosacch
2 xenopus lae
6 borrelia bu
9 neisseria m
2 salmonella
9 rickettsia
9 rickettsia
9 rickettsia
9 rickettsomyc
1 saccharomyc
8 flavobacter
1 streptococc
2 mycoplasma
0 streptococc
9 escherichia
                                                                                                                                                                                                                                                           7 borrelia ga
4 treponema p
2 bacillus su
1 borrelia bu
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Result No.

Score

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P29724; 083339;
101-APR-1993 (Rel. 25, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updathembrane lipoprotein tmpC precursor (Membra
                                                   Venter J.C.;
"Complete genome sequence spirochete.";
Science 281:375-388(1998).
                                                                                            Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J. Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J. Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garlan Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.
                                                                                                                                              STRAIN-NICHOLS;

WEDLINE-9833270; PubMed-9665876;

Fraser C.M., Norris S.J., Weinstock G.M.,
                                                                                                                                                                                                     MEDLINE=91372962; PubMed=1894360; Schouls L.M., van der Heide H.G.J., van Embden J.D.A.; Schouls L.M., van der Heide H.G.J., van Embden J.D.A.; "Characterization of the 35-kilodalton Treponema pallidum pallidum recombinant lipoprotein TmpC and antibody respons lipidated and nonlipidated T. pallidum antigens."; Infect. Immun. 59:3536-3546(1991).
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-NICHOLS; MEDLINE-91372962;
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Bacteria; Spirochaetales;
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                    SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS.
                                           SUBCELLULAR
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          Bacillus subtilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM STRAIN=168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Membrane;
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                    membrane protein
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SEQUENCE FROM N.A.

STRAIN-ATCC 35210 / B31;

MEDLINE-98065943; PubMed-9403685;

MEDLINE-98065943; PubMed-9403685;

Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K.

Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., van Yugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman Utterback T., Watthey L., McDonald L., Artiach P., Bowman Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hickey J.C.;

Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ojaimi C., Davidson B.E., Saint-Girons I., Old I.G., "Conservation of gene arrangement and an unusual organization genes in the linear chromosomes of the Lyme disease spirochaet Borrella burgdorferi, B. garinii and B. afzelii.", Microbiology 140:2931-2940(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94327086; PubMed-8050720;
Simpson W.J., Cieplak W., Schrumpf M.E.,
"Nucleotide sequence and analysis of the
encoding the immunogenic P39 antigen.";
FEMS Microbiol. Lett. 119:381-388(1994).
                                                                                                                                                                                                                                                 use by non-profit institute. There are no rest modified and this statement is not removed. Usage hy continues requires a license arrange.
                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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[5]
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"Heterogeneity of BmpA (P39) among European isolates burgdorferi sensu lato and influence of interspecies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
MEDLINE-98010210; PubMed-9350727;
InterPro; IPRO03760; Bmp.
Pfam; PF02608; Bmp; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
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burgdorferi.":
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NCBI_TaxID=139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clin.
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; U49938; AAC44713.1; -.
; X61517; CCAA57237.1; -.
; AEC01143; AAC66758.1; -.
; L35050; AAC41402.1; -.
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                                                                                                                                                                                                                                       email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                BELONGS TO THE BMP FAMILY OF LIPOPROTEINS.
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RC STRAIN=CLIP 11262 / Serovar 6a;

RC STRAIN=CLIP 11262 / Serovar 6a;

RX MEDLINE=21537279; PubMed=11679669;

RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

RA Charbit A., Chetheuani F., Couve E., de Daruvar A., Dehoux P.,

RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

RA Domann E., Dominguez-Bernal G., Duchaud E., Durant I., Dussurget O.,

RA Entlan K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,

RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

RA Jones L.-M., Keerst U., Kreft J., Kunst F., Kurapkat G.,

RA Maddeno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H.,

RA Moddeno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H.,

RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
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Best Local Similarity 26.9%;
Matches 101; Conservative 5:
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TCSA_LISIN
                                                                                                                                                                                                                                                                                                           01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
CD4+ T cell-stimulating antigen precursor.
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Pred. No. 0.000
58; Mismatches
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A -> T (I
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-> A (IN STRAIN 212).

-> T (IN STRAIN B31).

-> I (IN STRAIN B31).

-> P (IN REF. 3).

-> P (IN REF. 3).
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SEQUENCE FROM STRAIN-PBI;

N.A.

MEDLINE-98010210;

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Hauser

PubMed-9350727; er U., Wilske B.;

Borrelia garinii. Bacteria; Spirochaetales; NCBI\_TaxID=29519;

Spirochaetaceae;

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Best Local Sim
Matches 101;
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031362;
15-DEC-1998 (Rel. 3
15-DEC-1998 (Rel. 3
15-DEC-1998 (Rel. 3
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LIPID
SEQUENCE
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SIGNAL
                                                                                                            Basic membrane
                                                                                                                                                                                        BORGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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SIMILARITY: BELONGS
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PS00013; PROKAR_LIPOPROTEIN; 1.
Membrane; Lipoprotein; Signal; PROBABLE.
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Pred.
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Best Local 9
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15-DEC-1998 (Rel. 37, Created)
01-MAR-2002 (Rel. 41, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
CD4+ T cell-stimulating antigen precur
TCSA OR LM01388.
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                                                                                                                                                                                                                                                  Listeria monocytogenes.
Bacteria; Firmicutes; Bacillus/Staphylococcus
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J. Clin. Microbiol. 35:2752-2758(1997).
J. Chen. Microbiol. Attached to the membrane by a lipid anchor
     STRAIN=EGD-e / Serovar
MEDLINE=21537279; PubMe
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                                                                                                      SEQUENCE FROM N.A.
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L., M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoss N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
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STRAIN-85E0-1167;
MEDLINE-96096448; PubMed-7500019;
Sanderson S., Campbell D.J., Shastri N.;
"Identification of a CD4+ T cell-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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InterPro; IPR003760;
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                                                -SLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAG-FEFGKKSATVYLGIKD
                                                                                                    DKGQQIASSMYSSGVDVIFHAAGGTGNGVFAE-AKNLKKKDPSRAVWVIGVDRDQWDEGK
                                                                                                                                                                                                                                      AIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQ---DTSTK
                                                                                                                                                                                                                                                                                                                                                                                                                    GTDGYNYLQSASEADYK-----TNLNTAVRSDYDLIYGIGYKLKDAIEEVSKQKPKNQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGEITSVDSSTAELEGKYSSLANTNKNVWVLS-----GFQHGDAFTRWLK-IPENKQ
VTANDGKDYNVTLTSEIKRVDIAV----EDLAT----
                                                                                                                                                        ERLEQIASKDKPS----TLLAVAGPLTEIFSDIIANQNDR----
                                                                                                                                                                                                           KVGFVGGVKGTVIDRFEAGFTAGVKA--
                                                                                                                                                                                                                                                                                                                                                              LFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRS
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PEO250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL591979; CAC99466.1; S80336; AAB35725.2; A
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1 22 PRO
23 357 CD
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23
357 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROBABLE.
CD4+ T CELL-STIMULATING ANTIGEN.
N-ACYL DIGLYCERIDE (PROBABLE).
MW; 83605B8B6419C8D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 168; DB 1;
Pred. No. 0.0016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal; Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                           ------VNPNAQIDVQYANDFAKA
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RAKAGDFPGGTK - - - IEYGLDK
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BMPA_BORAF
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                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                 VARIANT
VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                          VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X81516; CAA57236.1; --
EMBL; X97237; CAA65876.1; --
EMBL; X97239; CAA65878.1; --
EMBL; X97241; CAA65880.1; --
InterPIO; IPRO03760; Bmp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-PRO, PWDDI, PLE, AND PLJ7;
MEDLINE-98010210; PubMed-9350727;
Roessler D., Hauser U., Wilske B.;
"Heterogeneity of BmpA (P39) among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BMPA_BORAF
031280; 031
                                                                                                                                                                                                                                                                                                      LIPID
VARIANT
                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02608; Bmp; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Basic membrane protein A precursor (Immunodominant antigen P39).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          serodiagnosis."
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burgdorferi sensu lato and influence of
                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Clin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=29518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borrelia afzelii.
                 165
                                                                          105
                                             83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Probable).
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clin. Microbiol. 35:2752-2758(1997) FUNCTION: NOT KNOWN; IMMUNOGENIC F
TEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTD-FIAGYLAGIKAWNLKNS:| :| | | | | | | | | | | | |
                                                                     TNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYK 164
                                                                                                                             GLNMAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSST----AELEGKYSSLAN 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                            AGSNLIWLIGYKFSDV-AKAVSLQNSEMKYAI----IDPVYSNEPIP-ANLVGMTFR
                                                                                                   GIPKVSLVIDGTFDDKSFNESALNGVKKLKEEFEIELVLKESSTNSYLSDLEG----LKD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAVGLSE-----HQDNISKDVLAKVE---EYKQKIVDGD-----IKVPEKP 357
                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           031281;
                                                                                                                                                                                                                                                                                                                                                   Membrane; Lipoprotein;
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                                                                                                                                                          7.7%;
nilarity 23.3%;
Conservative 6
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18
125
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214
214
258
268
268
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                                                                                                                                                             68
'
                                                                                                                                                                                                                                          PROBABLE.

BASIC MEMBRANE PROTEIN A.

N-ACYL DIGLYCERIDE (PROBABLE A -> S (IN STRAIN PLE).

I -> T (IN STRAIN PLJ7).

A -> P (IN STRAIN PLJ7).

A -> P (IN STRAIN PLJ7).

I -> V (IN STRAIN PLJ7).

I -> V (IN STRAIN PLJ7).
                                                                                                                                                     Score 166; DB
Pred. No. 0.007
68; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                 1BEABDF8CBA06FB4 CRC64;
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                                                                                                                                                                        DB 1;
.002;
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                                                                                                                                                             143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usage
                                                                                                                                                                                    Length
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                                                                                                                                                           Indels
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variability
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BMPD_BORBU
ID BMPD_B
AC Q44743
AC Q44743
AC Q44743
AC Q44743
DT 15-DEC
DT 16-OCT
DE Basic
GN BABDL
GN BMPD C
OS BOTTEL
OC BACTER
OX NCBL_1
RN (1)
RN SEQUEN
RR RAMAM
RAMAM
RAMAM
RAMAM
RA PETET
RX MEDLII
RX GENO
CC -1- S
CC -1- S
CC -1- S
CC Use
CC USE
CC MODII
CC OT SE
CC USE
CC This
CC OT SE
CC THIS
CC MEDLI
DR EMBL;
DR EMBL;
DR FABB;
DR FABB;
DR FABB;
DR PROSI
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                                                                                                                                             entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gw Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hansc van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujli C., Cotton M.D., Horst K., Roberts K., Hatch Smith H.O., Venter J.C.,
                                                                                 EMBL; U35450; AAC43984.1; EMBL; AE001144; AAB91505.
                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBLE the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and if entities requires a license agreement (See http://www.isb-sihentities requires a license agreement (See http://www.isb-sihentities.
                                                                                                                                                                                                                                                                                                                                                                             burgdorferi.";
Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-ATCC 35210
MEDLINE-98065943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96178617; PubMed=8606088; Ramamoorthy R., Povinelli L., Philipp M.T.; Ramamoorthy R., Povinelli L., Philipp M.T.; Molecular characterization, genomic arrangement, and bmpb, a new member of the bmp class of genes encoding proteins of Borrelia burgdorferi."; Infect. Immun. 64:1259-1264(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Basic membrane protein BMPD OR BB0385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q44743;
15-DEC-1998
                                                                  TIGR; BB0385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borrelia burgdorferi (Lyme disease spirochete).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                             InterPro; IPR003760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96178617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic sequence of a Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134
                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS
                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Attached
                                                                                                                                                                                                                                                                                                                                        (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPEMPDKQPDKQQESLDKLITD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGK----LINYGLKEGVVGFV-----RNPKMIPFEV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NQ--NDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFE 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -KDIKIFSQYIGSFSDLEAG---RSVATKMYSDGI-----DIIHHAAGLGGIGAIEVA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKKTKITTDKI----EINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQEGAFLTGYIAAKV-----SKTGKIGFLGGIEGDIVDAFRYGYEAGAKYAN----
                                                                                                                                             s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spirochaetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                    disease spirochaete,
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SEQUENCE
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Q45010; P94249; Q44857;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
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SIGNAL
                 SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.F.
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.
Dougherty B., Tomb J.-F., Fleischmann R.D., Salzberg S.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S.,
                                                                                                                                                                                                        MEDLINE=97132632; PubMed=8978084;
Aron L., Toth C., Godfrey H.P., Cabello F.C.;
"Identification and mapping of a chromosomal oburgdorferi containing genes expressed in vive FEMS Microbiol. Lett. 145:309-314(1996).
                                                                                                                                                                                                                                                                                                                                                                                                 Simpson W.J., Cieplak W., Schrumpf M.E., "Nucleotide sequence and analysis of the encoding the immunogenic P39 antigen."; FEMS Microbiol. Lett. 119:381-388(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94327086; PubMed-8050720;
Simpson W.J., Cieplak W., Schrump
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; S
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N-ACYL DIGLYCERIDE (PROBABLE).
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-i- FUNCTION: NOT KNOWN; IMMUNOGENIC PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PFOSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95111614; PubMed-7812434; Ojaimi C., Davidson B.E., Saint-G
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Nature 390:
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DKQQESLDKLITD
                      YGLKEGVVGFV----RNPKMISF--
                                           LGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDKQP
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                                                                                    IGVDTDQSLYYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVY
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TE; PS00013; PROKAR_LIPOPROTEIN; 1.
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                                                                                                                                                                                                                                                                                           85;
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use by non-profit institutions as long as its content
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"A survey of the Mycoplasma
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                                                                           ANKHFGLNMAIVTAG--GTVNDNSFNQSGWEAIQQLGALTGG-EITSVDSSTAELEGK--
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(Rel. 40, Last annotation
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AR LOCATION: Attached
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Hu P.-C., Bott K.F., Hutchison
he Mycoplasma genitalium genome
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                                                                                                                           Score 152.5;
Pred. No. 0.02
14; Mismatches
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N-ACYL DIGLYCERIDE (POTENTIAL).
; 14A8FA31BB7E0928 CRC64;
                                                                                                                                                                                                                                                                                                 POTENTIAL
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                                                                               X MEDLINE-98065943; PubMed-9403685;
X MEDLINE-98065943; PubMed-9403685;
A Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.P.
A Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K.,
A Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
A Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Han
A Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Han
A Van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
A Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
A Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatc
B Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97132632; PubMed=8978084;
Aron L., Toth C., Godfrey H.P., Cabello F.C.;
"Identification and mapping of a chromosomal ge
burgdorferi containing genes expressed in vivo.
FEMS Microbiol. Lett. 145:309-314(1996).
                       Nature 390:580-586(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and DNA sequence analysis of bmpC, potential membrane lipoprotein of Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aron L., Alekshun Cabello F.;
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Bacteria; Spirochaetales; S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                     SEQUENCE FROM N.A.
MEDLINE=87260937; PubMcd=3037534;
Laddaga R.A., Chu L., Misra T.K., Silver
"Nucleotide sequence and expression of th
                                                                                                                                                                                                          Staphylococcus aureus Plasmid pI258.
                                                                                                                                                                                                                                                        MERA.
                                                                                                                                                                                                                                                                                                                                                                        MERA_STAAU
P08663;
                                                                                                                                                                                                                                                                                                                                                                                                                         STAAU
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                                                                                                                                                           Bacillus/Staphylococcus
                                                                                                                                                                                      Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                              Mercuric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVQKNPLNLFWLI-GYRFSDL-----SVKLSYERPDIYYGIIDAFDYGDIQ--VPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGITGLGVYDAAKELGPKYYVIGLNQDQSYI---APQNVITSIIKDIGKVIYSISSEYI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGPLTEIFSDIIANQNDR-YLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGIFYANPKLRLVSKKAPSLFD------
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                                                                                                                                                                                                                                                                              reductase
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(Rel. 06, Last sequence update)
(Rel. 41, Last annotation update)
ductase (EC 1.16.1.1) (Hg(II) redu
                     sequence and expression of the
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23.7%;
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                                                                                                                                                           Bacillus/Clostridium grous group; Staphylococcus
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PROBABLE.

BASIC MEMBRANE PROTEIN C

N-ACYL DIGLYCERIDE (PROE

N-ACYL DIGLYCERIDE (PROE

N-Y-L (IN STRAIN 297).

V-> L (IN STRAIN 297).
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Pred. No. 0
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plasmid pI258
                                                                                                                                                                                                                                                                                                                                                                                                547
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                        mercurial-resistance
                                                                                                                                                                                 group;
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MBL outstation -
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Query Match
Best Local
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Pfam; PF00070; pyr_redox; 1.
Pfam; PF02852; pyr_redox_dim; 1.
PRINTS; PR00368; FADPNR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L29436; ANA98245.1; -.
PIR; E29504; E29504.
HSSP; P11959; 1EBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the property of the p
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-!- FUNCTION: RESISTANCE TO HG(2+) IN BACTERIA APPEARS TO BE GOVERNED BY A SPECIALIZED SYSTEM WHICH INCLUDES MERCURIC REDUCTASE. MERA PROTEIN IS RESPONSIBLE FOR VOLATILIZING MERCURY AS HG(0).

-!- CATALYTIC ACTIVITY: Hg + NADP(+) + H(+) - Hg(2+) + NADPH.

-!- COPACTOR: FAD.

-!- SUBUNIT: HOMODIMER.

-!- MISCELLANEOUS: THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BOND.
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PROSITE; PS50846; HMA_2; 1.
PROSITE; PS00076; PYRIDINE_REDOX_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
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InterPro; IPR001934; HMA.
InterPro; IPR001815; Hg_reductase.
InterPro; IPR001100; pyr_redox.
279
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                                                                          GSGYIAAELGQMFHNLGTEV---TLMQRSERLFKTYDPEISEAIDESLTEQGLNLITGVT
                                                                                                                                                                                                                                                                                                    LAKKF----PSDPTKRSAIVIGGGISPAVTDFIAG-----YLAGIKAWNLKNSDKKTKI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKIPENK ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGAKVAMVERGTVGGTCVNIGCVPSKTMLRAGEINGLAQNNP----FTGLQTSTGAADL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSGWEAIQQLGALTGG---EITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRW 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELSDDQIEKAKQNISAAGYQPGEEESQPSENSVDFNRDGDYDLLIIGSGGAAFSAAIKAN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKSADNQNKQITDVSKISGLVNERKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSF--N 67
                                                                                                                                                                                                                          IDDKTIQVNGQNITSKS-FLIATGASPAVPE-IPGMNEVDYLTSTSALELKEVPQRLAVI 256
                                                                                                                                                                                                                                                                                                                                                                                  AQLTEQKDGLVSQMRQEK - - - -
                                                                                                                                                ----TTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDII----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR00945; HGRDTASE.
PR00411; PNDRDTASEI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -QLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASF 179
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-- IGVDTDQSLVYTKTKNKFFTSILKNLGYSV---FSVLSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 136; DB 1
Pred. No. 0.26;
54; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REDOX-ACTIVE.

FAD (FLAVIN PART) (B'HG(2+) (POTENTIAL).

HG(2+) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAD (ADP PART) (PROBABLE).
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                                                                                                                                                                                                                                                                                                                                                                               -----YIDL---IEEYGFDLIRGEASF 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an M1 strain of Streptococcus pyogenes. Proc. Natl. Acad. Sci. U.S.A. 98.4658-4663(2001).

-I- CATALYTIC ACTIVITY: DIPEPTIDASE FAMILY U34.
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE006627; AAK34726.1; -.
Hydrolase; Dipeptidase; Complete proteome.
SEQUENCE 498 AA; 55499 MW; B9394DC94C19AE4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probable dipeptidase B (EC PEPDB OR SPY2066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-SF370 / ATCC 700294 / Serotype
MEDLINE-21192684; PubMed-11296296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
STRAIN-SF370 / ATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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 212
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LAGIKAWNLKNSDKKTKIT-
                                   ASEDVEKVAKKAKSYTEVDGKFH---IAKSYNPPLNDANRSRSFSG-----
                                                                                                                                                                                                            NMAIVTAGGTVND-----
                                                                                                                                                                                                                                                                            KETTKEEKSADNON------KOITDVSKISGLVNERKSEIMAAKADANKHFGL 50
                                                                                                       GNIVTLADKD-GIWYMEILSGHQYVA-----IKFPDDKYAVFPNTFYLGHVDFNDKENTI
                                                                                                                                      GKYSSLANTNKNVW----VLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVI 153
                                                                                                                                                                          SMS-ATVSASANDAIQKIDPYVKNGLAESSMTSVILPSVKTAREGVALIAKIVTEKGAAE
                                                                                                                                                                                                                                            KDNPAGEKWKDLSNGFEYPLPEHSYRYSAIPDVTPNKGVYDE------AGFNE-FGV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATVGLTEQQAKEKGYDVKTSVLPLDAVPRAL 464
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                                                                    PTGRYINLTYKTEEAGWLAGYANASFLAKKF--PSDPTKRSAIVIGGGISPAVTDFIAGY
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                                                                                                                                                                                                                                                                                                                                  Similarity
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20.5%;
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Last annotation updat
B (EC 3.4.-.-).
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                                                                                                                                                                                                                                                                                                              65;
                                                                                                                                                                                                        NSFNQSGWEAIQQLGALTGGE----ITSVDSSTAELE 96
                                                                                                                                                                                                                                                                                                                                Score 129; DB Pred. No. 0.61;
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-TDKIEINLGFDVQDTSTKER---
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                                                                                                                                                                                                                                                                                                              175; Indels 144;
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n S.P.,
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                                                                                                       225
                                                                                                                                                                          171
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Search completed: July 18, 2002, 15:30:21 Feb time: 68 sec

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Database :
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Gapop 10.0 ,
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length DB	BDB	ID	Description
1	693.5	32.2	457	2	Q48902	Q48902 mycoplasma
N	552	25.6	461	16	Q98QL5	Q98q15 mycoplasma
ω	391	18.1	465	N	Q9X775	Q9x775 mycoplasma
4	384.5	17.8	428	N	052311	052311 mycoplasma
ۍ	382.5	17.7	428	N	Q9RGX5	
σ	379.5	17.6	428	N	032417	032417 mycoplasma
7	379	17.6	429	N	Q9RGX6	_
8	379	17.6	429	N	Q9RGX4	_
9	377.5	17.5	428	N	Q9RGX7	Q9rgx7 mycoplasma
10	374.5	17.4	428	N	Q9RGX3	Q9rgx3 mycoplasma
11	373.5	17.3	428	ຎ	Q9R3N6	Q9r3n6 mycoplasma
12	228	10.6	349	N	Q9EV91	Q9ev91 clostridium
13	220.5	10.2	350	16	Q99ZH4	Q99zh4 streptococc
14	203.5	9.4	350	16	Q9CFM9	Q9cfm9 lactococcus
15	202	9.4	350	16	Q97RH0	Q97rh0 streptococc
16	192	8.9	357	16	Q97L60	

45	44	43	42	41	40	39	38	37	36	35	34	S S	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
126.5	127	127	131.5	132	132.5	133.5	134	137.5	140	143	143.5	145	148	150	156	157	160	161	161	162.5	164	168	168.5	170	173	174	178.5	182
5.9	5.9	5.9	6.1	6.1	6.1	6.2	6.2	6.4	6.5	6.6	6.7	6.7	6.9	7.0	7.2	7.3	7.4	7.5	7.5	7.5	7.6	7.8	7.8	7.9	8.0	8.1	8 . 3	8.4
894	2045	912	1558	326	330	1786	539	889	379	353	243	264	329	524	325	339	325	339	339	525	347	341	516	264	357	342	359	348
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Q91962 moraxella c	Q9a0k5 streptococc		℧		Q926d6 rhizobium m	Q9uOpO plasmodium	Q9pq10 ureaplasma	Q91961 moraxella c	Q9rsq4 deinococcus		orrelia			ureaplas	borrelia	borrelia		087960 borrelia bu	Q9s6cl borrelia bu	Q9pqr5 ureaplasma	Q9ak42 streptomyce	Q9fd93 borrelia bu	Q9prd3 ureaplasma	ъ	Q92bw7 listeria in		7	Q9ak41 streptomyce

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                                                                                                                                                                                               Query Match 32.2:
Best Local Similarity 39.0:
Matches 168; Conservative
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SIGNAL
CHAIN
SEQUENCE
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
AG 243-5 PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-96163149; PubMed-8551970;
Ushio S., Iwaki K., Taniai M., Ohta T., Fukuda S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycoplasmataceae; Mycoplasma
NCBI_TaxID=2094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma arginini.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metastatic promoting activity of a novel molecule, Ag 243-5 derived
from Mycoplasma and the determination of the complete nucleotide
65 SFNQSGWEAI----QQLGALTG-GEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGD 119
                                                               28 ETDKEGKII-----RIFD----NSFVKDRQAEIEKA-----KNFDFNTVLLTAGGTVQDK 73
                                                                                                                                   u
                                                                                                      ETTKEEKSADNQNKQITDVSKISGLVNERKSEIMAAKADANKHFGLNMAIVTAGGTVNDN 64
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26
457 AA;
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                                                                                                                                                                                                                                                                                                                                                                  25 POTENTIAL.
457 AG 243-5 PROTEIN.
50789 MW; 9AEEAB11620CB22F CRC64;
                                                                                                                                                                                                                               32.2%;
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Last annotation updat
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                                                                                                                                                                                                  Score 693.5; DB 2;
Pred. No. 1.9e-32;
1; Mismatches 141;
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                                                                                                                                                                                                   Query Match
Best Local S
Matches 133
                                                                                                                                                                                                                                                                                                                         Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145.
EMBL; AL445564; CAC13519.1;
MypuList; MYPU_3460; -
InterPro; IPR003760; Bmp.
Pfam; PF02608; Bmp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-UAB CTIP;
MEDLINE-21267165; PubMed-11353084;
Chambaud I., Hellig R., Ferris S., B.
Moszer I., Dybvig K., Wroblewski H.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q98QL5;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
ABC TRANSPORTER XYLOSE-BINDING LIPOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma pulmonis.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasmataceae;
NCBI_TaxID=2107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYPU_3460.
                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of the murine
                    108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134
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                                                        83
                                                                                          62
                                                                                                                                                                                                 / Match 25.6%;
Local Similarity 31.2%;
les 133; Conservative (
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   NVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTEN-VIPTGRYINLTYKTE
                                                                                                                          AQNPNKTNSNLDSSKITDLLSQKEVTETQKIVENKIKQASLETQK-----VVLITADGNI 82
                                                      DDKSFNQQVYESQKTLKDFVDKAYKSQNKEAENQHKLDNYINSAVKDLEQNYKVALDRGY 142
                                                                           NDNSFNQSGWEAIQQLGALTGGEITS----
                                                                                                                                                             ADNONKQIT--DVSKISGLVNER-----KSEIMAAKADANKHFGLNMAIVTAGGTV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKQPDKQQESL 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEM---P
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                                                                                                                                                                                                                                                                                                          proteome.
                                                                                                                                                                                                                                                                                             461 AA;
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                                                                                                                                                                                                                                                                                           51096
                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                   82;
                                                                                                                                                                                                 Score 552; DB
Pred. No. 2.9e-
32; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barbe V., Si
., Viari A.,
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                                                                                                                                                                                                 DB 16;
2.9e-24;
les 161;
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E.P.C.,
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Query Match
Best Local Similarity
Matches 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                       malp product of Mycoplasma fermentar of bacterial lipoproteins."; Infect Immun 67:6213-6216(1999). EMBL; AJ132423; CAB43718.1; -. InterPro; IPR003760; Bmp. 1 Pfdm; PF02608; Bmp; 1 Signal; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9X775;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
P48 MEMBRANE LIPOPROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                       CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplasma agalactiae.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20002620;
Rosati S., Pozzi S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-M7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycoplasmataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "P48 major surface antigen of Mycoplasma agalactiae is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             439 TNGDLE
                                                                                                                                                                                                                  VTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSSTAELEGK------YSSL 102
                                    LAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPL-
                                                                                                                                  ANTIKNVWVLSGFQHGDAFTRWLKIPENK-QLFTEKNIIILGIDWT----DTENV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDRYLIGVDTDQSLYYKTKNKFFTSILKNLGYSVFSVLSDLYT-----KKSNSRNL 333
                                                                                                                                                                                          ITDEGSVHDESFNQSGWEAVHKVSYELGLDKAQV-SGNKNLRNKVYEPKKGQLLEAYKNA 128
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                                                                                                                                                                                                                                                                                                                                                                   23
465 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               397
                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S., Robino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=10531294;
S., Robino P., Montinaro B., Conti
                                                                                                                                                                                                                                                                                                                                                                     22
465 F
51149 MW;
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                                                                                                                                                                                                                                                                                           18.1%;
31.2%;
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                                                                                                                                                                                                                                                                      Score 391; DB 2;
Pred. No. 5.9e-15;
6; Mismatches 128
                                                                                                                                                                                                                                                                                                                                                                   P48 MEMBRANE LIPOPROTEIN.; 60AD5448CFE03C96 CRC64;
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ
EMBL, AF036106; AAB99740.1; -
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Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
"Differential posttranslational processing confers intraspecies variation of a major surface lipoprotein and a macrophage-activating lipopeptide of Mycoplasma fermentans.";
Infect. Immun. 67:760-771(1999).
EMBL; AF099211; AAD16395.1; -.
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                                                                                                                                                                                                                                                                                                                                                                     NERKSEIMAAKADANKH------FGLNMAIVTAGGTVNDNSFNQSGWEAI
                                                                      VDIADTSLEGNDKKL-ATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQPDKQQE
                                                                                                                                                                                             SFGGGAFPGVTTENEGFAKGILYYNQKH--KSSKIYHTSPVKLDSGF----TAGEKMNT
                                                                                                                                                                                                            VIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQ
                                                                                                                                                                                                                                           TEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI 194
                                                                                                                                                                                                                                                                                                             QQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLF 134
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RLEAIISAIN 424
                       SLDKLITDIN
                                                                                               ILTSVLKHIKQAVYETLLDLILEKEEGYKPYVVKDKKADKKWSHFGTQ
                                                                                                                                             VINNVLSSTPADVKYNPHVILSVAGPAT--FETVRLANKGQYVIGVDSDQGMI--QDKDR
                                                                                                                                                              IAS-----KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNK
                                               IGVAENHFSNTEEQAKINNKIKEAIKMFKE----LPEDFVKYINSDKALKDGNKIDNVSE
                                                                                                                     FFTSILKNLGYSVFSVLSDL------YTKKSNSRNLAGFEFGKKSATVYLGIKDRF
                                                                                                                                                                                                                                                                                               KAINKQTGIEINSVEPS-SNFESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREEL
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428 AA;
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(TTEMBLTel. 13, Last sequence update)
(TTEMBLTel. 17, Last annotation update)
aCTIVATING LIPOPROTEIN-404 PRECURSOR.
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47835 MW;
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27.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 382.5; DB 2; Pred. No. 1.6e-14;
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MACROPHAGE ACTIVATING LIPOPROTEIN-404;

D03F0F47EA2B1460 CRC64;
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                                                                                               -KEKW
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032417;
01-JAN-1998
01-JAN-1998
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98022661; PubMed=9359703; Matsumoto M., Takeda J., Inoue N., Hara T., Ha Nagasawa S., Akedo H., Seya T.; "A novel protein that participates in nonself malignant cells by homologous complement."; Nat. Med. 3:1266-1270(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplasma fermentans.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                         Patent number JP1997157295-A/1
17-JUN-1997. KAGAKU GIJUTSU SH
EMBL; D64083; BAA23530.1; -.
EMBL; AB026157; BAA77211.2; -.
INTERPRO; IPR003760; Bmp.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Seya T., Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-98241611;
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Submitted
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Matsumoto M., Nishiguchi M., Kikkawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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NCBI_TaxID=2115;
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ILTSVLKHIKQAVYETLLDLILEKEEGYKPYVVKDKKADKKWSHFGTQ
                        FFTSILKNLGYSVFSVLSDL----
                                            VINNVLSSTPADVKYNPHVILSVAGPAT - - FETVRLANKGQYVIGVDSDQGMI -
                                                                                           SFGGGAFPGVTTFNEGFAKGILYYNQKH--KSSKIYHTSPVKLDSGF----
                                                                                                               VIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQ
                                                                                                                                       ERNQIKIIGIDF-DIETEYKW--FYSLQFNIKESAFTTGYAIASWLSEQ---DESKRVVA
                                                                                                                                                                                     KAINKQTGIEINNVEPS-SNFESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREEL
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                                                                                                                                                                                                                                 NNDESNISFKEKDISKYTTTNANGKQVVKNAELLKLKPVLITDEGKIDDKSFNQSAFEAL
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NCE 428 AA;
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LO M., Seya T.
Ed (APR-1999)
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26.7%;
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Last annotation updat
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Pred. No. 2.4e-14;
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Best Local Similarity
Matches 117; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-SP11554; PubMed=9916088;

Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;

"Differential posttranslational processing confers intraspecies variation of a major surface lipoprotein and a macrophage-activating lipopeptide of Mycoplasma formentans.";

Infect. Immun. 67:760-771(1999).

EMBL; AR099210; AAD16394.1; -.

InterPro; IPR003760; Bmp.

Pfam; PR05608; Bmp.; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal; Lipoprotein.
SIGNAL 1
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01-DEC-2001
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WIGVAENHFSNTEEQAKINNKIKEAIKMFKELPEDFVKYINSDKVLK---
                                                                                                VINNVLSSTPADVKYNPHVILSVAGPAT -- FETVRLAANKGQYVIGVDSDQGMI--QDKD
                                              IAS-----KDKPSTLLAVAGPLTEIFSDI-IANQNDRYLIGVDTDQSLVYTKTKN
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                       FVDIADTSLEGNDKKL-ATEAISEAKKEF----
                                                                       KFFTSILKNLGYSVFSVLSDL-----
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                                                                                                                                                                                                                                                   KAINKQTGIEINNVEPS-SNFESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREEL
                                                                                                                                                                                                                                                                                                     NNDESNISFKEKDISKYTTTNANGKQVVKNAELLKLKPVLITDEGKIDDKSFNQSAFEAL 86
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MACROPHAGE ACTIVATING LIPOPROTEIN-404

; B6D09A8812AC3171 CRC64;
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                                                                     YTKKSNSRNLAGFEFGKKSATVYLGIKDR 352
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Best Local Similarity 26.9
Matches 116; Conservative
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Q9RGX4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-9911554; PubMed-9916088; Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.; Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.; "Differential posttranslational processing confers intraspecies variation of a major surface lipoprotein and a macrophage-activating lipopeptide of Mycoplasma fermentans."; Inject. Immun. 67:760-771(1999).
EMBL; AF099212; AAD16396.1; -.
InterPro; IPR003760; Emp.
Pfam; PF02608; Bmp. 1.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Lipoprotein. SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycoplasmataceae;
NCBI_TaxID=2115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Bacteria; Firmicutes; Bacillus/Clostridium
415
                                                     411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI-TTDKIEINLGPDVQDTSTKERLEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NNDESNISFKEKDISKYTTTNANGKQVVKNAELLKLKPVLITDEGKIDDKSFNQSAFEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NERKSEIMAAKADANKH------FGLNMAIVTAGGTYNDNSFNQSGWEAI
                                                                                                            WIGVAENHFSNTEEQAKINNKIKEAIKMFKE----LPEDFVKYINSDKALKDGNKIDNVS
                                                                                                                                                                                                                         RILTSVLKHIKQAVYETLIDLILEKEEGYKPYVVKDKKADKKWSHFGTQ
                                                                                                                                                                                                                                                                               KEFTSILKNLGYSVFSVLSDL------YTKKSNSRNLAGFEFGKKSATVYLGIKDR
                                                                                                                                                                                                                                                                                                                                         VINNVLSSTPADVKYNPHVILSVAGPAT --FETVRLAANKGQYVIGVDSDQGMI--QDKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFGGGAFPGVTTFNEGFAKGILYYNQKH--KSSKIYHTSPVKLDSGF----TAGEKMNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERNQIKIIGIDF-DIETEYKW--FYSLQFNIKESAFTTGYAIASWL@GQ---DESKRVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAINKQTGIEINNVEPS-SNFESAYNSALSAGHKIWVLNGFKHQQSXKQY--IDAHREEL
                                                  ESLDKLITDIN
                                                                                                                                                               FVDIADTSLEGNDKKL-ATEAISEAKKEFEEKTKTIPAEEVRKTLE::PEMPD-KQPDKQQ 410
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429 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                     421
                                                                                                                                                                                                                                                                                                                                                                       -KDKPSTLLAVAGPLTEIFSDI-IANQNDRYLIGVDTDQSLVYTKTKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma
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47933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 379; DB 2;
Pred. No. 2.6e-14;
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MACROPHAGE ACTIVATING LIPOPROTEIN-404

B6D08CF975AC3171 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154;
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                                                                                                                                                                                                                         KEK
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GN DOT AC

OPRGX3 PRELIMINARY; PRT; 428 AA.
OPRGX3;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence up
O1-JUN-2001 (TrEMBLrel. 17, Last annotation
MACROPHAGE ACTIVATING LIPOPROTEIN-404 PRECUE

PRECURSOR

update)

update)

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RESULT
Q9RGX7
RESULT
Q9RGX3
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STRAIN-II-29/1;
STRAIN-II-29/1;
STRAIN-II-29/1;
MEDLINE-9911554; PubMed-9916088;
Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt
"Differential posttranslational processing con
variation of a major surface lipoprotein and
r lipopeptide of Mycoplasma fermentans.";
Lipopepti
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Best Local Similarity
Matches 110; Conserv
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Q9RGX7;
01-MAY-2000
01-MAY-2000
01-JUN-2001
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycoplasmataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycoplasma fermentans. Bacteria; Firmicutes;
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                                                                                                                                                       390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WVLNGFKHQQSIKQY--IDAHREELERNQIKIIGIDF-DIETEYKW--FYSLQFNIKESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAG
                                                                                                                                                       PEDFVKYINSDKALKDGNKIDNVSERLEAIISAIN
                                                                                                                                                                                                                           PAEEVRKTLEIPEMPD-KQPDKQQESLDKLITDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LANKGQYVIGVDSDQGMI---QDKDRILTSVLKHIKQAVYETLLDLILEKEEGYKPYVVKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDL-----YTKKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YHTSPYKLDSGF----TAGEKMNTYINNYLSSTPADYKYNPHYILSVAGPAT--FETYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI
                                                                                                                                                                                                                                                                                                           KKADKKWSHFGTQ-----
                                                                                                                                                                                                                                                                                                                                                                                   NSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKL-ATEAISEAKKEFEEKTKTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -TTDKIEINLGFDVQDTSTKERLEQIAS-------KDKPSTLLAVAGPLTEIFSDII
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0 (TremBLrel. 13, Last sequence update)
1 (TremBLrel. 17, Last annotation updata
ACTIVATING LIPOPROTEIN-404 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycoplasma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ME:
                                                                                                                                                                                                                                                                                                       KEKWIGVAENHFSNTEEQAKINNKIKEAIKMFKE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 377.5;
Pred. No. 3.
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MACROPHAGE ACTIVATING LIPOPROTEIN-404

, D6B69C0BA969CFE1 CRC64;
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Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muhlradt P.F., Wise K.S. essing confers intraspect
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16;

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RESULT
Q9R3N6
ID Q9
AC Q9
AC Q9
DT 01
DT 01
DT 11
DT 01
CN MA
OC My
OC BA
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Q9R3N6;
01-MAY-2000
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Mycoplasma fermentans.
Bacteria; Firmicutes; Bacillu
Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2115;
[1]
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SEQUENCE
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                                                                                                                                   LIPOPROTEIN
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EMBL; AF099213; AAD16397.1; -.
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SIGNAL 1
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Bacteria; Firmicutes; Bacillus/Clostridium
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115; Conser
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MACROPHAGE ACTIVATING LIPOPROTEIN-404;

C7A536B409A60132 CRC64;
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STRAIN-PG18, M39A, AND M70B;

KMEDLINE-99115554; PubMed-9916088;

Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.

"Differential posttranslational processing confet of the confe
                                                                                                                                                                              Q9EV91 PRELIMINARY;
Q9EV91;
01-MAR-2001 (TrEMBLrel. 16, C
01-MAR-2001 (TrEMBLrel. 16, L
01-DEC-2001 (TrEMBLrel. 19, L
PUTATIVE SUBSTRATE BINDING LI
                                       Bacteria; Firmica
Clostridium.
NCBI_TaxID=1511;
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SEQUENCE FROM N.A. STRAIN-DSM 519T;
                                                                                                                       Clostridium
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LIPOPROTEIN PRECURSOR OF
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MACROPHAGE ACTIVATING LIPOPEPTIDE MALP-2.
; 59808324E218F03C CRC64;
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Q99ZH4;
01-JUN-2001
01-JUN-2001
01-DEC-2001
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an M1 strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

EMBL; AE006563; AAK34087.1; "...
InterPro; IPR001114; Adenylsucc_synt.
InterPro; IPR003760; Bmp.
InterPro; IPR003761; Peripla_BP_like.
InterPro; IPR003217; Tubulin.
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"Molecular analysis of the grd-operon encoded proteins of the reductase and thioredoxinsystem from Clostridium sticklandii." Arch. Microbiol. 175:8-18(2001).
EMBL; AJ276209; CAC14304.1; -.
InterPro; IPR003760; Bmp.
                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-SF370 / ATCC 700294 / SEROTYPE M.
MEDLINE-21192684; PubMed-1129696;
Feiretti J.J., McShan W.M., Ajdic D.J.,
                                                                                                                                                                                                                                          Streptococcus pyogenes. Bacteria; Firmicutes; E
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01-DEC-2001 (TrEMBLrel.
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Pfam; PF00533; Peripla Bp_like;
PROSITE; PS00227; TUBULIN; UNKN
Lipoprotein; Complete proteome.
SEQUENCE 350 AA; 36396 MW;
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                                                                    Bolotin A., Wincker P., Mauger S., Jaillon C
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic
lactis ssp. lactis III.403.";
Genome Res. 11.731-753(2001).
EMBL; AE006374; AAK05536.1; -.
Interpro; IPR003760; Emp.
Pfam; PF02608; Emp; 1.
                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-IL1403;
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Tettelln H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
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McDonald L.A., Feldblyum T.V., Angluoli S., Dickinson T., Hickey i
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                                                                                                                                                                                                         Science 293:498-506(2001).
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TIGR; SP0845; -.
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Query M Best Lo Matches	SULT CO	22266666666666666666666666666666666666
Match Local Simi nes 98;	SULT 1  18-961-083-8  Sequence 8, Application of the patent No. 6159469  GENERAL INFORMATION:  ADPLICANT: Choi e  TITLE OF INVENTION  NUMBER OF SEQUENCE  CORRESPONDENCE ADD  ADDRESSEE: Human  STREET: 9410 Ke  CITY: ROCKVILLE  STATE: MATYLAND  COMPUTER READABLE:  MEDIUM TYPE: DI-  COMPUTER: HP Ve-  OPERATING SYSTEM  APPLICATION NUMB  FILING DATE:  CLASSIFICATION NUMB  FILING DATE:  ATTORNEY/AGENT INF  NAME: BFOOKES,  REGISTRATION FOR SEQ  SEQUENCE CHARACTER  LENGTH: 328 ami  TYPE: amino aci  STRANDEDNESS: S  TOPOLOGY: linea  MOLECULE TYPE: pr-  O8-961-083-8	108 108 107.5 107.5 107.6 107.1 107 107 107 107 107 107 107 107 107 10
uilarity Conserva	961-083-8 961-083-8 961-083-8 961-083-8 PPLICANT: Choi et. al. ITLE OF INVENTION: Streptoce UMBER OF SEQUENCES: 452 ORRESPONDENCE ADDRESS: ADDRESSE: Human Genome Sc STREET: 9410 Key West Aven CITY: ROCKVILLE STAYE: MATYLAND COUNTRY: USA ZIP: 20850 OMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.51 COUNTRY: USA ZIP: 20850 OMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS Ve. SOFTWARE: ASCII Text URRENT APPLICATION NUMBER: US/08/ FILING DATE: APPLICATION NUMBER: US/08/ FILING DATE: F	
9. 25. tive	ation US/089 ON: i et. al. iON: Strept NOES: 452 ADDRESS: uman Genome Key West Av LE FORM: LE FORM: Diskette, 3 Vectra 486/ TEM: MSDOS TEM: UMBER: US/0 N: 435 ON DATA: UM	3418 3418 3418 3418 1964 2052 607 607 703 753 1579 11912 11912 11912 11912 11912 11912 11912
740;	7,08961 7,08961 7,52 1,52 1,52 1,52 1,52 1,53	♡ C C C C C C C C C C C C C C C C C C C
Score 202; DB 4; Le Pred. No. 5.6e-11; 55; Mismatches 145;	### Procedure preumoniae Antigens ### Sciences, Inc. ### Avenue  3.50 inch, 1.4Mb storage  6/33 storage  8 version 6.2  708/961,083  **N: **Fig. 1.4 storage  8: **Phistorage  9: **Phistorage  1: **Phistorage  2: **Phistorage  3: **Phistorage  3: **Phistorage  4: **Phistorage  5: **Phistorage  6: **Phistorage  7: **Phistorage  8: **Phistorage  1: **Phistorage  2: **Phistorage  3: **Phistorage  4: **Phistorage  7: **Phistorage  1: **Phistorage  1: **Phistorage  1: **Phistorage  1: **Phistorage  1: **Phistorage  1: **Phistorage  2: **Phistorage  3: **Phistorage  4: **Phistorage  1: **Phistorage  1: **Phistorage  2: **Phistorage  3: **Phistorage  4: **Phistorage  1: **Phistorage  1: **Phistorage  2: **Phistorage  3: **Phistorage  4: **Phistorage  1: **Phistorage  1: **Phistorage  2: **Phistorage  3: **Phistorage  4: **Phistorage  4: **Phistorage  1: **Phistorage  2: **Phistorage  3: **Phistorage  4: **Phistorage  4: **Phistorage  5: **Phistorage  6: **Phistorage  7: **Phistorage  8: **Phistorage  1: **Phistorage  1: **Phistorage  1: **Phistorage  1: **Phistorage  1: **Phistorage  2: **Phistorage  3: **Phistorage  3: **Phistorage  3: **Phistorage  3: **Phistorage  4: **Phistorage  3: **Phistorage  4: **Phistorage  3: **Phistorage  4: **Phistorage  4: **Phistorage  4: **Phistorage  4: **Phistorage  5: **Phistorage  6	US-08-755-587-16 US-08-639-501-2 US-09-044-946-2 US-09-044-908-2 US-08-790-912-3 US-08-790-912-2 US-08-646-790-95-6 US-08-646-273-25 US-08-646-273-36 US-08-646-273-36 US-08-646-273-36 US-08-646-273-36 US-08-646-273-36 US-08-646-273-36 US-08-646-273-36 US-08-646-273-36 US-08-723-927-8 US-08-723-927-8 US-08-723-927-8 US-08-728-470-10 US-08-719-641-10
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RESULT 2
US-08-396-957A-5
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                TELEFAX: (212) 751-684
TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/664
FILING DATE: 05-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/487
FILING DATE: 05-MAY-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                 REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: FLOPPY
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: NEW YORK
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                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/020,245 FILING DATE: 19-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                          (212) 751-6849
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ANTIGENIC PROTEINS AND
GENES ENCODING SAME OF BORRELIA BURGDORFERI.
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US-08-396-957A-4
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                                                                                                                                                                                                                                                        Sequence 4, Application US/08396957A Patent No. 5780041
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Best Local Similarity 26.9%;
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                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: SIMPSO
                                                                                                               TITLE OF INVENTION: ANTIGENIC PROTEINS TITLE OF INVENTION: GENES ENCODING SAN NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
COMPUTER READABLE FORM:
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NAME/KEY:
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                            COUNTRY:
                                                         CITY: NEW YORK STATE: NEW YOR
                                                                                             STREET:
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STRAIN: Sh-2-82
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
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STRANDEDNESS: sir
TOPOLOGY: unknown
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                    10154
                                                       NEW YORK
                                                                                               345 PARK AVENUE
                                       USA
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                                                                                                                                                           GENES ENCODING SAME OF
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Pred. No. 1.1e-08;
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                                                                                                                                                                             BORRELIA BURGDORFERI.
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COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS

MEDIUM TYPE:

FLOPPY DISK

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Best Local :
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/46
PRIOR DATE: 05-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELLEPAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 07/664,731
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189
                                                                 143
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                                                                                                                                                               115 FQHGD-AFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAG 173
                             233 KI----EINLGFDVQDTSTKERLEQTASKDKPSTLLAVAGPLTEIFSDIIANQ--NDRYL 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL TYPE:
CELL LINE:
                                                                                                                                  93
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                                                                                                                                                                                                                                                                                  / Match 7.5%; Score 161; DB 1; Lenyth 339;
Local Similarity 22.8%; Pred. No. 4.5e-07;
                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION METHOD: OTHER INFORMATION: p3
OTHER INFORMATION: se
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STRAIN: Sh-2-82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/0 FILING DATE: 19-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                 59 GTVNDNSFNQSGWEAIQQLGALTGGEITSVDSST----AELEGKYSSLANTNKNVWVLSG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: p39'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
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STRANDEDNESS: si
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YIGSFADLEAGRSVATRMYSDEID------IIHHAAGLGGIGAIEVAKELGSGHYI 238
                                                                                             YANASFLAKKEPSDPTKRSAIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITTD 232
                                                                                                                                YRFSDVAKVAALQNPDMKYAI------IDPIYSNDPIP-ANLVGMTFRAQEGAFLTG
                                                                                                                                                                                                 GTFDDKSFNESALNGVKKVKEEFKIELVLKESSSNSYLSDLEG----LKDAGSDLIWLIG
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unknown
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01-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                   sequence.
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                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                            Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,412
                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 35
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Chromosomally-Encoded Membrane TITLE OF INVENTION: Protein of Borrelia Burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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140 NS-LAIKFRNEEAAFLAGYIAAKMSRKE------KIGFLTGPMSEHLKDFKFGFK 187
                                 156 GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIG---GGISPAVTDFIAGYL 212
                                                                                                    100 SSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGI----DWTDTENVIPT 155
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                                                                     92 EVQKNPLNLFWLI-GYRFSDL-----SVKLSYERPDIYYGIIDAFDYGDIQ--VPK 139
                                                                                                                                       34 VLAHGSFYDKGYNQSVHDGVVKLRDNFGIKLITKSLRPYPIEGKRLLTVDE--AMTEDAY 91
                                                                                                                                                                        55 VTAGGTVNDNSFNQSGWEAIQQLG------ALTGGEITSVDSSTAELEGKY
                                                                                                                                                                                                           Match 6.6%;
Local Similarity 23.4%;
Les 83; Conservative 54
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CLASSIFICATION:
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Rochester
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                                                                                                                                                                                                         Score 143; DB 4; L
Pred. No. 2.4e-05;
A· Mismatches 131;
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CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 889
TYPE: PRT
ORGANISM: Moraxella catarrhalis
US-09-336-447A-15
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US-09-336-447A-15
; Sequence 15, Application US/09336447A
; Patent No. 6310190
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Best Local 9
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APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
    612
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KOTEATDALNKASSENTONI - - EDLAAYNELODAYAKOOTEATDALNKASSENTONIAKN
                                                                                                                   YTKKSN-SRNLAGFEFGKKSATVYLG--IKDRFVDIADTSLEGNDKKLA--
                                                                                                                                                                                               LAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLYYTKTKNKFFTSILKNLGYSVFSVLSDL
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                                       --TEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDKQPDKQQESLDK--------
                                                                            IDQKADLTKDIKALESNVEEGLLDLSGRLIDQKADIAQN--QANIQDLAAYNELQDQYAQ
                                                                                                                                                            LNLSGRLIDQKADIDNNINHIYELAQQQDQHSSDIKT-----LKKNVEEGLLELSGHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GWEAIQQLG---ALTGG--EITSVDSSTA-----ELEGKYSSLA------
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                                                                                                                                                                                                                                                                                                                                           I---NLTYKTEEA-------GWLAGYANASFLAKKFPSDPTKRSAIVIGGG-ISPA 203
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APPLICANT: DAULHE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERVTHROCYTIC STA
FILE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER FILING DATE: 1996-06-12
EARLIER APPLICATION NUMBER: FR 95/07007
EARLIER APPLICATION NUMBER: FR 95/07007
SARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
SOPTWARE: PATENTIN VET. 2.0
SEQ ID NO 8
LENGTH: 1786
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08973462B Patent No. 6191270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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                                                                                LTDKMIDAVEESIEISSDSKEETESIKDKEKDVSLVVEEVQDNDMDESVEKVLELKNM--
                                                                                                           IKDRFVDIADTSLE-GNDKKLATEAISEAKKE----FEEKTKTIPAEEVRKTLEIPEMPD 403
                                                                                                                                                                                                                                                                                                  DKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIF---SDIIANQNDRYLIG
                                                                                                                                                                                                                                                       EHVEQNVYVDV------DVPAMKDQFLGILNEAGGLKEMFFNLEDVFKSESD--VIT 1129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEKSADNQNKQITDVSKISGLVNERKSEI------MAAKADANKHFGLNMAIVTAGG 59
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-----EEELMKDAVEINDI 1239
                                        KQPDKQQESLDKLITDINNL 423
                                                                                                                                                                     VEEIKDEPVQKEVEKETVSIIEEMEENIVDVLEE---EKED
                                                                                                                                                                                                             VDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTGRY----INLTYKTEEAGWLAG 173
                                                                                                                                                                                                                                                                                                                                          ------KVDLNENVVSSILDNIENMKEGLLNKLENISSTEGVQETVT 1080
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US-09-308-375-2 ; Sequence 2, Application US/09308375 ; Patent No. 6300117

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; LENGTH: 2285
; TYPE: PRT
; ORGANISM: Bacillius subtilis
US-09-308-375-2
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: Sequence 2, Application US/08409995

: Patent No. 5646259
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                       Patent No. 5640227

Patent No. 5640227

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: St. Geme III, Joseph W.
APPLICANT: St. Geme III, Joseph W.
AITILE OF INVENTION: Haemophilus Adhesion Proteins
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
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Best Local Similarity
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TITLE OF INVENTION: Proteases From Gram-Positive Organisms
FILE REFERENCE: GC394-PCT
CURRENT APPLICATION NUMBER: US/09/308,375
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: EP9719636.4
EARLIER APPLICATION NUMBER: EP9719636.4
EARLIER FILING DATE: 1997-09-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.5%; Score 117.5; Dest Local Similarity 19.1%; Pred. No. 0.04; Matches 112; Conservative 75; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                               734
                                                                                                                                                                    683
                                                                                                                                                                                                                                                                                 228 KITTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANQND-RYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349 TEDADEGKGLYTAKDVI--DAVNKTGWRIKTTDANGQNGDFATVASGTNVTFASGNGTTA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 TVEFLSADTETTTVTVDSKENGKRTEVKIGAKTSVIKEKDGKLFTGKANKETNKVDGANA 348
794
                                                                                                                       324 YTKKSNSRNLAG---FEFGKKSATVYLGIKDRFVDIADTS------LEGN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 LAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 LFTEKNII--ILGIDWTDT-------ENVIPTGRYI-----NLTYKTEEAGW 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: doul
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 -----MAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSST----AELEGKYS 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 TKEEKSADNQNKQITDVSKISG-------LVNERKSEIMAAKA--DANKHFGLN- 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVTAKGLYTALNSLSWTTTAAEADGGTLDGNASEQEVKAGDKVTFKAGKNLKVKQEGANF
                                                                                                                                                                                                                                                                                                                                        TKDGISAGGQSVKNVVSGLKKFGDANFDPLTSSADNLTRQNDDAYKGLTNLDEKGTDKQT 636
IAKSGFELGLADEA -- DAKRAFDDKTKALSA -- -- GTTEIVNAHDK 833
                      -----DKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDK 404
                                                                                                                                                                                                                                                    PVVADNTAATVG-DLRG-----LGWVISADK-----TTGGSTE-YHDQVRNANEVKFK 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVTNGTDGITVKYDAKVGDGLKLDGDKIAADTTALTVNDGKNANNPKGKVADVASTDEKK
                                                                                  YYSKEDIDLTTGQPKLKDGNTVAAKYQDKGGKVVSVTDNTEATITNKGSGYVTGNQVADA
                                                                                                                                                                  SGNGINVSGKTVNGRREITFELAKGEVVKSNEFTVKETNGKETSLVK------VGDK 733
                                                                                                                                                                                                         IG-----TSILKNLGYSVFSVLSDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08685467 Patent No. 6060059
                                                                                                                                                                                                                                                                                                                                                                                                                                                               uery Match
st Local Similarity
tches 112; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A - C
TELECOMMUNICATION I INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/409,995
FILING DATE: 24-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: St. Geme III, Joseph W. APPLICANT: Barenkamp, Stephen J.
                                                                                                                                                             467
577 TKDGISAGGQSVKNVVSGLKKFGDANFDPLTSSADNLTKQNDDAYKGLTNLDEKGTDKQT
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TOPOLOGY: un
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME:
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                                                                                                                LAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDF-----
                                                                                                                                                                                                                                                                        SLANTNKNVWVLSGFQHGD-------AFTRWLKI-------PENKQ 132
                                                                            TYSLQDAL-----TGLTSITLGTGNNGAKTEINKDGLTITPANGAGANNANTISV
                                                                                                                                                       LVTAKGLVTALNSLSWTTTAAEADGGTLDGNASEQEVKAGDKVTFKAGKNLKVKQEGANF 526
                                                                                                                                                                                             LFTEKNII -- ILGIDWTDT------ENVIPTGRYI-----NLTYKTEEAGW 170
                                                                                                                                                                                                                                 TVTNGTDGITVKYDAKVGDGLKLDGDKIAADTTALTVNDGKNANNPKGKVADVASTDEKK 466
                                                                                                                                                                                                                                                                                                                                                                                         TVEFLSADTETTTVTVDSKENGKRTEVKIGAKTSVIKEKDGKLFTGKANKETNKVDGANA 348
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                                                                                                                                                                                                                                                                                                                                                  -----MAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSST----AELEGKYS 100
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Four Embarcadero Center, Suite 3400
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, Robin M.
38,304
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; ORGANISM: Haemophilus influenzae
US-09-377-155-32
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; Sequence 32, Application US/09377155
; Patent No. 6197312
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NUMBER OF SEC. THE STATE OF SEC. THE SEC. 
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CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 199-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILLING .... 33
NUMBER OF SEQ ID NOS: 33
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nes 112; Conserv
PVVADNTAATVG-DLRG-----LGWVISADK-----TTGGSTE-YHDQVRNANEVKFK
                                                                KITTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANQND-RYL
                                                                                                                                       {\tt TKDGISAGGQSVKNVVSGLKKFGDANFDPLTSSADNLTKQNDDAYKGLTNLDEKGTDKQT
                                                                                                                                                                                                                   -------IAGYLAGIKAW---
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                                                                                                                                                                                                                                                                                                                                                                                                                                  LYTAKGLYTALNSLSWTTTAAEADGGTLDGNASEQEVKAGDKYTFKAGKNLKVKQEGANF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------MAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSST----AELEGKYS 100
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JENNINGS, Michael Paul
MOXON, E. Richard
WENTION: NOVEL SURFACE ANTIGEN
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19.1%; Pred. No. 0.04;
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; MOLECULE TYPE:
US-08-913-942-2
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                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILIG DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Vance, Dall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: FOUL CITY: San Francisco
STATE: California
Thited Stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/4031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Flehr Hohbach Test Albritton & Herbert ADDRESSEE: Flehr Hohbach Test ADDRESSEE: Flehr Hohbach T
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APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: VANCE, DOLLY A.
REGISTRATION NUMBER: 39,054
REFERENCE, DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                  7 TKEEKSADNQNKQITDVSKISG-----
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                                                                                                TVEFLSADTETTTVTVDSKENGKRTEVKIGAKTSVIKEKDGKLFTGKANKETNKVDGANA 348
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                               -----MAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDS3T----AELEGKYS 100
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94111-4187
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29-DEC-1997
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TVEFLSADTETTTVTVDSKENGKRTEVKIGAKTSVIKEKDGKLFTGKANKETNKVDGANA 348

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TEDADEGKGLVTAKDVI--DAVNKTGWRIKTTDANGQNGDFATVASGTNVTFASGNGTTA 406

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                                                                                                           ; ORGANISM: Haemophilus influenzae US-09-669-974-32
                                                                                                                                                                SOFTWARE: Pater
SEQ ID NO 32
LENGTH: 1098
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  Query Match
Best Local Similarity
Matches 112; Conserv
                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR TILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
                                                                                                                                                       TYPE: PRT
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                      5.5%;
Score 117.5; DB 4;
Pred. No. 0.04;
75; Mismatches 170;
                                          Length
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                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Haemophilus influenzae US-09-268-347-44
                                                                                                                                                                                                                                                                                    Query Match 5.5%;
Best Local Similarity 19.1%;
Matches 112; Conservative 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: LOOSMOTE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038-880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 44, Application US/09268347 Patent No. 6335182
                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT EILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
TO ID NO 44
LENGTH: 1098
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
 467
                                                                       407
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                                  LFTEKNII--ILGIDWTDT------ENVIPTGRYI-----NLTYKTEEAGW 170
                                                                                                       SLANTNKNVWVLSGFQHGD-----AFTRWLKI-----
                                                                                                                                                                                                              TVEFLSADTETTTVTVDSKENGKRTEVKIGAKTSVIKEKDGKLFTGKANKETNKVDGANA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YYSKEDIDLTTGQPKLKDGNTVAAKYQDKGGKVVSVTDNTEATITNKGSGYVTGNQVADA 793
LVTAKGLVTALNSLSWTTTAAEADGGTLDGNASEQEVKAGDKVTFKAGKNLKVKQEGANF
                                                                                                                                          TEDADEGKGLYTAKDVI - DAVNKTGWRIKTTDANGQNGDFATVASGTNVTFASGNGTTA 406
                                                                                                                                                                                                                                               TKEEKSADNQNKQITDVSKISG------LVNERKSEIMAAKA--DANKHFGLN- 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTKKSNSRNLAG---FEFGKKSATVYLGIKDRFVDIADTS------LEGN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGNGINVSGKTVNGRREITFELAKGEVVKSNEFTVKETNGKETSLVK------VGDK
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                                                                    TVTNGTDGITVKYDAKVGDGLKLDGDKIAADTTALTVNDGKNANNPKGKVADVASTDEKK 466
                                                                                                                                                                           -----MAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSST----AELEGKYS 100
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                                                                                                                                                                                                                                                                                     75;
                                                                                                                                                                                                                                                                                                    Score 117.5; D
Pred. No. 0.04;
                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                    170;
                                                                                                                                                                                                                                                                                                                      Length 1098
                                                                                                                                                                                                                                                                                    Indels 229;
                                                                                                       ----PENKQ 132
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-923-992A-4
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                                                                                                                       TELEFAX: (202) 371-254 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                 CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA FC
TITLE OF INVENTION: Streptococcal Beta
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,992A
FILING DATE: 05-SEP-1997
                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino aci
                                                                                                                                                              REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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ZIP: 200
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STATE: D.C
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                                                                                                                                                                                                                           NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                            amino acid
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                                                                                  1104 amino acids
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Best Local Similarity Matches 85; Conserv

Conservative

5.4%; Score 116.5; DE 17.9%; Pred. No. 0.051; tive 78; Mismatches 2 78;

DB 4; 208;

Length 1104; Indels

103;

Gaps

13;

Query Match

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RESULT 15
US-09-074-658-75
; Sequence 75, Application US/09074658
; Patent No. 6184371
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                                                      TELEFAX: (416) 595-11
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acid
TYPE: amino acid
                                                                                            REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Quijun Wang
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN
NUMBER OF SEQUENCES: 78
                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     543 SAQQELEKLEKAI -- KELMEQPEIPSNPEYGIQKSIWESQKEPIQEAITSFNKI 594
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                                                                                                                                                     NAME: Stewart, Michael I REGISTRATION NUMBER: 24,973
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## ALIGNMENTS

MHP3; antigen; vaccine; enzootic mycoplasma pneumonia; antibody; immunoassay; immunotherapy; anti-idiotypic antibody.

07-SEP-2001 AAU01859;

(first entry)

AAU01859 standard; Protein;

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Mycoplasma hyopneumoniae MHP3 antigen.

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Matches 451; Conserv
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                                                                                                                                                                                                                             The sequence represents Mycoplasma hyopneumoniae a recombinant MHP3 antigen lacking the first 28 amino acids (the putative signal sequence). MHP3 antigen and its fragments are useful in manufacturing a vaccine for treating or preventing a disease or disorder in an animal, especially pig, caused by M. hyopneumoniae infection e.g. enzootic mycoplasma pneumonia. The mhp3-encoded proteins may be used as immunogens to generate antibodies which immunospecifically bind such an immunogen. The antibodies generated against the antigen are useful in diagnostic immunoassays, passive immunotherapy and generation of anti-idiotypic antibodies. Mhp3 proteins may also be used in immunoassays, e.g. to detect or measure in a biological sample from a vaccinated or potentially infected test animal the presence of antibodies to the antigen, and thus to monitor the immune response and/or to diagnose
                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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rapy; anti-idiotypic antibody; mutein.
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16-SEP-1987;
11-DEC-1987;
04-JAN-1988;
16-MAR-1990;
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                                                   DNA encoding a regression-associated antigen from M. is used to obtain prods. for diagnosis, localisation
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                                                              ndakdnekasl 414
                                                                                DKQPDKQQESL 441
                                                                                                                 YLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEM---P
                                                                                                                                                                                                                                                                                                             ykgisddfvgvsnstvadadkvkaqeflneatadfkkqiqanpt-nyksvlgiptmlind
                                                                                                                                           DKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDII--ANQNDRYLIGV
                                                                                                                                                                                                                           etdkegkii----rifd----nsfvkdrgaeieka----knfdfntvlltaggtvgdk 48
                                                                                                                                                                                                                                                                                                                                                                             ETTKEEKSADNQNKQITDVSKISGLVNERKSEIMAAKADANKHFGLNMAIVTAGGTVNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1995-040317/06.
DB; AAQ79124.
                                                                                                                                                                 DTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGK----KSATV
                                                                                                                                                                                                                                                  AGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKITT
                                                                                                                                                                                                                                                                       efpkflkqtdsngkkysdllaekkviivavdwdlskedkdlikaghfisllykteeagfi
          standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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         protein;
                                                                                                                                                                                                                                                                                                                                                                                                          30.2%; Score 694.5; DB 16; 39.0%; Pred. No. 4e-44;
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          448
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Best Local S
Matches 171
                                                                                                                                                                                                                                                                                                                                                                                 Regression-associated antigens may be used in diagnostic tests, vivo imaging, for monitoring the course of therapy or for therap purposes, eg active immunisation protocols in cancer patients or delivery systems by binding the drug to monoclonal or monospecific polyclonal Ab showing specific immunoreactivity with the Ag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Peptide
Protein
                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour regression-associated antigens and antibodies used in diagnostic tests, monitoring course of there
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene encoding the 43 kd regression-associated Mycoplasma hyorhinis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; ; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy in cancer patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasma
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                                                                                                    174
                                                                                                             180 VIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGY
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                                                    234
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                                                                                                                                                                                                                                                                        14 GLVFPLSAIAT-ISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNERKSEIMAAKADA 72
ssvvdaikksnkdtkyligvdtdqskifppa-tvfft-iekhlgrtiyevitdiwlkked
                                                              LAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLT
                                                                                                {\tt likaghfisllyktee} agfiagy as {\tt skflaykfpndeakrtiapfggghgagvtdfiagf}
                                                                                                                                                                                                                                                EIFSDII--ANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSN
                                                                                                                                                                 SSLANTNKNVWVLSGFQHGDAFTRWLKIPEN-----KQLFTEKNIIILGIDW----TDTEN 179
                                                                                                                                                                                                             NKHFGLNMAIVTAGGTVNDNSENQSSWEAI----QQLGALTG-GEITSVDSSTAELEGKY 127
                                                                                                                                                  knflngnknvwiltgfqqgqefpkflkqtdsngkkysdllaekkviivavdwdlskedkd
                                                                                                                                                                                               -knfdfntvlltaggtvqdksfnqsiweavlehydqiekttnldrvsqetnnqseligky 113
                                                lagiakynndnptakvtisdnninidtgf-isndftatfingivnks--slvlpvvgslt
                                                                                                                                                                                                                                                                                                  28.5%; Score 655; DB 10; al Similarity 37.4%; Pred. No. 4e-41; 171; Conservative 89; Mismatches 149;
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1..25
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est Local Similarity
Matches 126; Conserv
                                                                                                                                                                                                                                                                                                                         This sequence represents the inflammatory cytokine of the invention. The inflammatory cytokine can be used in a drug, which useful for the treatment of thrombocytopaenia.
                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                             New inflammatory cytokine inducer gene treatment of thrombocytopaenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-281057/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inflammatory cytokine inducer.
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lyynqkh--ksskiyhtspvkldsgf-----tagekmntvinnvlsstpadvkynphvil
                       KAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQIAS-----KDKPSTLL
                                                              GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISFAVTDFIAGYLAGI 243
                                                                                                                                          vvknael-----lklkpvlitdegkiddksfnqsafealkainkqtcleinnveps-snf 106
                                                                                                                                                       EIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAEL 123
                                                                                                                                                                                IKWNKFLGLGLVFPLSAI-ATISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNERKS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIPAEEVRKTLEIPEM-PDKQPDKQQESLDKLITDIN 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s-flgsfrsfkltnaanatvykgisd-flgvsnstvadadkvkaqefln-atadfkkqiq 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRNLAGFEFGK----KSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTK
                                              --fyslqfnikesafttgyaiaswlseq---deskrvvasfgggafpgvttfnegfakgi
                                                                                             esaynsalsaghkiwvlngfkhqqsikqy--idahreelernqikiigidf-dieteykw
                                                                                                                   EGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPT
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                                                                                                                                                                                                                                                                                                                                                                       3; Page 16-17; 22pp; Japanese
                                                                                                                                                                                                                                                                                                    428
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytokine inducer; thrombocytopaenia; therapy
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                                                                                                                                                                                                                                       17.2%; Score 394.5; DB 20; 26.8%; Pred. No. 1.6e-21; Live 101; Mismatches 174;
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RESULT ANW227727
ID ANW227727
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Best Local Sim
Matches 127;
                                                                                                                                                    This sequence is a membrane protein designated M161Ag. Oligonucleotide probes for the cDNA were designed from putative N-terminal M161Ag pepti sequences isolated from P99 cells. M161Ag can be used in the developmen of a leukaemia treating agent.
                                                                                                                           Sequence
                                                                                                                                                                                                                      Claim 1; Fig 1; 6pp; Japanese.
                                                                                                                                                                                                                                                    Membrane protein M161Ag treating agent
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                                                                                                                                                                                                                                                                                               N-PSDB; AAT75133
                                                                                                                                                                                                                                                                                                            WPI; 1997-369470/34.
                                                                                                                                                                                                                                                                                                                                      (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                   05-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                             05-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     402 SEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQPDKQQESLDKLITDINK 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 IKWNKFLGLGLVFPLSAI-ATISAGCWDKETTKEEKSADNQNKQIT----DVSKISGLVN 59
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mkkskkillgl-spiaailpavavsc----
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                                                                    Similarity
                                                                                                                           429
                                                        Conservative
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185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                    16.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "selenocysteine"
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                                                                                                                                                                                                                                                                 useful in development of leukaemia
                                                    96;
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                                                    Score 387.5; DB 18;
Pred. No. 5.4e-21;
6; Mismatches 174;
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           AAY81501 to AAY81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antiinflammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be used in vaccines and individually antipens.
and/or antigens. The ni
diagnostic assays. The
                                                                                                                                                  New Streptococcal protein, useful as a vaccine, pneumococcal diseases and for screening agents cor inhibiting expression of the protein -
                                                                                                                                                                                                                                             Gilbert CFG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus
                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                         27-JUL-1998;
19-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumococcal
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                                                                                                                                                                                                                                                                                                                                                     27-JUL-1999;
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                                                                                                        31-OCT-1996;
                                                                                                                                                                                                                                                                                                                           Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW55066 standard; Protein;
                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                             30-OCT-1997;
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                                                                                                                                                                                                                                                                     WO9818930-A2
                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae SP007
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                                                                                                                                                                                                                                                                                                                                                                              antigen; vaccine; infection;
tis media; meningitis.
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Pred. No. 5.1e-09;
5; Mismatches 149
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       can be useful in vaccines for inducing protective antibodies against pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein are used to detect corresponding antigens, to purify the protein are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
Enterococcus
detection; at
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                                                  Enterococcus
                                                                                                                     AAY00049;
                                                                                                                                                     AAY00049 standard; Protein;
                                                                                    20-APR-1999
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                                                                                                                                                                                                                                                                       KLATEAISEAKKEFEEKTKTIP 416
                                                                                                                                                                                                                                                                                                      stlkqvgttvkdi-----snkaergefpggq---vivyslkdkgvdlavtnlseegk
                                                                                                                                                                                                                                                                                                                                      SILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         liddvikdqknv-----asvtfadnesgylagvaaak----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSOPTKRSAIVIGGGI
                                                                                                                                                                                                                                                                                                                                                                         --ivyqvaggtgagvfaeakslnesrpenekvwvigvdrdqeaegkytskdgkesnfvlv
                                                                                                                                                                                                                                                                                                                                                                                                        PSTLLAVAGPL-TEIFSDIIANQNDR-----YLIGVDTDQSL--VYT----KTKNKFFT
                                                                                                                                                                                                                                                                                                                                                                                                                                        esevisrfeagfkagv----asvdpsikvqvdyag-sfg-daakgktiaaaqyaagad-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SPAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Page 50; 118pp; English.
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-avedakakildgsvkvp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328 AA;
 attenuation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                 faecalis;
                                                 faecalis antigenic polypeptide fragment EF021.
                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    represents a protein from Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNII
              infection; vaccine;
 antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding the Streptococcus pneumoniae protein
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                                                                                                                                                     339
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Pred. No. 3e-07;
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                 immune response; diagnosis;
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06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents an antigenic polypeptide fragment isolated from Enterococcus faecalis. The present invention describes isolated from E. faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-070095/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein activity.
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305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 ktaesgggkgda----ahsaviitdtggvddksfnqssweglqawgkehdlpegskgyay
                                                                                                                                                                                                                                                                                                                                                                    GIDWIDTENVIPTGRYINLIYKTEEAGWLAGYANASFLAKKFPSDPIKRSAIVIGGGISP : | : : | : : | : : | : : | : : | |
                                                                               ktkdgkednftltstlkgvgtavqdianraledk-----
                                                                                                                                                                                                              TLLAVAGPLTEIFSDII-----
                                      VDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD
                                                                                                                                                                   kgkalaaamyqngvdiifhasgatgqgvfqeakdlnesgsgdkvwvigvdrdqdadgky-
                                                                                                                                                                                                                                                         vvidrfqagfekgv-adaakelgkeitvdt---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                        -NKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRF
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97US-0044031.
97US-0046655.
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Pred. No. 1.2e-05;
1; Mismatches 139
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AAY00048
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06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                         by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids products from the present invention can also be used for screening
                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a protein isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused be used in vaccines for preventing or attenuating an infection caused be used in vaccines.
                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                 activity.
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                                                                                                                                                                                                                       61 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGA---LTGGE----
                                                                                              GIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISP
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DB; AAX20038.
 TLLAVAGPLTEIFSDII--
                                                      AVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPS
                                                                                  ddqidgkknv-----vsatfrdneaaylagvaaa-
                                                                                                                                                                                            ktaesgggkgda----ahsaviitdtggvddksfnqssweglqawgkehdlpegskgyay
                           vv1drfqagfekgv-adaake1gke1tvdt--------kyaasfadpa
                                                                                                                                                                 ITSVDSS--TAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIIL 170
                                                                                                                                       iqsndaadyttnidqavsskfntifgi----gyllkda-----issaadanpdtnfvli 134
                                                                                                                                                                                                                                                 tch 7.9%; al Similarity 25.4%; 104; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 100;
                                                                                                                                                                                                                                                                                                                                                              to identify agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                attenuation;
                                                                                                                                                                                                                                                                                                                      361 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              faecalis;
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97US-0044031.
97US-0046655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                   51;
                                                                                                                                                                                                                                                 Score 182; DB
Pred. No. 1.3e<sup>o</sup>
51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361
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                                                                                                                                                                                                                                                 DB 20;
..3e-05;
les 139;
 ANQUDR-YLIGVDTDQSL--VYT
                                                                                 -netktnkvgfvggeeg 179
                                                                                                                                                                                                                                                                           Length 361;
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                                                                                                                                                                                                                                                                                                                                                            faecalis protein
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Best Local S
Matches 101
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19-FEB-1993;
01-MAR-1995;
                                                                                                                                                                                        This represents the Borrelia burgdorferi antigenic protein p39 beta. The antigenic protein p39 alpha is immunoreactive with mammalian Lyme borreliosis serum. The Borrelia antigenic proteins p39 alpha and p39 beta are used in vaccines to protect against Lyme disease, as assay reagents to detect specific antibodies in the serum (diagnostic of Lyme disease), and to raise antibodies, either for diagnosis (by detecting disease), and to raise antibodies, either for diagnosis (by detecting
                                                                                                                                                                                the
                                                                                                                                                                                                                                                                          Example 6; Columns 31-34; 33pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW61758 standard; Protein;
                                                                                                                                            Sequence
                                                                                                                                                                   expression
                                                                                                                                                                                                                                                                                                             New antigenic for raising
                                                                                                                                                                                                                                                                                                                                                                                     Schwan TG,
                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US
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                                                                                 Local Sir
hes 101;
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             --LANTNKN---
                                                ANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAELEGKYSS---
                                 sskkikismlv---dgvlddksfnssaneallrikkdfpenieevfs--caisgvyssyv
                                                                                                                                                                                                                                                                                                                                                            1998-413001/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        borreliosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ktkdgkednftltstlkgvgtavgdianraledk...--fpggehlvy-glkdgg
                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                 AAV35685,
                                                                                                                                             341
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                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                              proteins from antibodies or
                                                                                                                                                                                                                                                                                                                                                                                                                                 91US-0664731.
90US-0487716.
93US-0020245.
95US-0396957.
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-VWVLSGFQHGDAFTRWLKIPENKQLFTEKNII--ILGIDWTDTENVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lyme
                                                                                                                                                                             antigen) or in screening agents
                                                                                                                                                                                                                                                                                                                                                  AAV35687
                                                                                                                                                                     proteins
                                                                                                                                                                                                                                                                                                                                                                                     ٤
                                                                                             7.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease.
                                                                                Score 179; DB
Pred. No. 2e-0
59; Mismatches
                                                                                   59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341
                                                                                                                                                                                                                                                                                                              Borrelia burgdorferi useful in vaccines for diagnostic detection of specific
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                                                                                             2e-05;
                                                                                                        DB 19;
                                                                                   123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha;
                                                                                                        Length 341;
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                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p39 beta;
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                                                                                   92;
                                                                                 Gaps
            181
                                    78
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          The invention relates to a novel secreted autostimulatory factor, interleukin-X (II-X), from an Epstein Barr virus (EBV)-carrying lymphoblastoid cell line. IL-X proteins can be used to enhance the growth of cells in vitro, or to grow primary human B cell cultures to facilitate
                                                                                         New IL-x polypeptides useful e.g. for enhancing the growth of cells vitro, for growing primary human B cell cultures to facilitate proliferation of these cell lines, as therapeutics or prophylactics, molecular weight standards
                                                                                                                                                                                    Blazar BA,
                                                                                                                                                                                                                                              08-AUG-1994;
11-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                              Misc-difference
proliferation
                                                                   Claim 1; Page 7; 16pp; English.
                                                                                                                                                                                                                                                                               16-JAN-2001; 2001US-0760541
                                                                                                                                                                                                                                                                                                       06-SEP-2001.
                                                                                                                                                                                                                                                                                                                             US2001019713-A1
                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interleukin-X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interleukin-X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU07352 standard;
                                                                                                                                                                                                                       (BLAZ/)
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                                                                                                                                                                                                           (WEBB/)
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)B; AAS11798.
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                                                                                                                                                                                                          BLAZAR B A.
WEBB A C.
                                                                                                                                                                                    Webb AC;
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 of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IL-X)
                                                                                                                                                                                                                                                                                                                                                                                                                                              IL-X; autostimulatory factor; Epstein
; B cell.
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93US-0026132
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 these cell
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therapeutics
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or prophylactics,
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Best Local Similarity 27.3%;
Matches 50; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     molecular weight standards, as inert proteins in an assay, or in the detection of antibodies that are immunoreactive with IL-X. Nucleotide sequences encoding the peptides could be used to produce recombinant peptides or they could be used as probes or primers for diagnostic and/or analytical polymerase chain reaction (PCR) procedures, or as DI or RNA sizing standards. The present sequence represents the amino ac sequence of IL-X.
                                                                                                                                                                                                                                                                                                                                                            Polymerase chain reaction; PCR; primer; open reading frame; ORF; antigen; 39-alpha; 39-beta; serum; human; Lyme patient; p39-beta; p39-alpha; promoter; -10; -35; ribosomal binding site; RBS.
                                                                          New Borrelia burgdorferi protein and DNA isolates - used detection of Lyme borreliosis infection and in prodn. of antibodies and vaccines
                                                                                                                                                                                                                                                     05-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                   P39-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                            17-DEC-2001
11-MAY-1993
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                                                                                                                                                                                                                                                                                                                                   Borrelia burgdorferi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR33280 standard;
                                                 Disclosure; Page 36-39; 69pp; English.
                                                                                                                                 N-PSDB; AAQ34672.
                                                                                                                                             WPI; 1993-017799/02.
                                                                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 TSILKNLGYSVFSVLSDL-----YTKKSNSRNLAGFEFGKKSATVYLGIKDRFVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 GGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQIA
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Pred. No. 2.1e-05;
7; Mismatches 56;
                                                                                                                                                                                                   SERVICE
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The sequences given in AAR31013 and AAR33280 represent the B. burgdorferi proteins P39-alpha and P39-beta. The DNA encoding proteins was isolated by polymerase chain reaction (PCR) using

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C beta indicates that these genes have 628 similarity.

C Sovernment-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent
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Best Local S
Matches 100
                                                  Polymerase chain reaction; PCR; primer; open reading frame; ORF; antigen; 39-alpha; 39-beta; serum; human; Lyme patient; p39-beta; p39-alpha; promoter; -10; -35; ribosomal binding site; RBS.
                  Borrelia burgdorferi
                                                                                                                                  P39-alpha
                                                                                                                                                                        17-DEC-2001
11-MAY-1993
                                                                                                                                                                                                                                  AAR31013;
                                                                                                                                                                                                                                                                      AAR31013 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        site at www.derwent.com/dwpi/updates/ntis_us.html.)
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                                                                                                                                                                                                                                                                                                                                                                                                      KTIPAEEVRKTLEIP 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASK--DKPSTLLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a-----igfirgmkgnivdafr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTGRYINLTYKTEEAGWLAGYANA--SFLAKKFPSDPTKRSAIVIG--GGISPAVTD-FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sdldnlkrngsdliw-lvgymltda--sllvssenpki--sygiidpiygddvqipenli 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --LANTNKN----VWVLSGFQHGDAFTRWLKIPENKQLFTEKNII--ILGIDWTDTENVI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGPLTEI-FSDIIANQND-RYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ygyesgakyan-kdieliseysnsfsdvdig-----rtiaskmyskgidvihf 221
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(first entry)
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Pred. No. 6.8e-05;
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CC primer sequences given in AAQ34673-76. This DNA contained two open CC reading frames (ORF). It was therefore concluded that the P39 antigen CC which has been previously described is not one protein but two, 39-alpha CC and 39-beta. The P39 signal appears to be enhanced when both genes CC calculated molecular weight of 36.926 kD. The protein with a CC gene which is reactive with serum from human Lyme patients. The ORF CC of gene 2 has been designated p39-beta. This genes' ORF starts 116 CC nucleotides downstream of p39-alpha and encodes a protein of 341 amino CC acids (37.506 kD). The promoter located 5' of p39-alpha appears to be present with classic -10 and -35 regions whereas p39-beta lacks a CC recognisable promoter sequence. Both genes have putative ribosomal CC with a TAA codon. Comparing the gene sequences of p39-alpha and p39-alpha code indicates that these genes have 62% similarity.

CC (Note: Revised entry submitted to correct the patent number format of CC granted patent numbers. For further information please visit the Derwent valve.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Borrelia burgdorferi protein and DNA isolates - used detection of Lyme borreliosis infection and in prodn. of antibodies and vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                       The sequences given in AAR31013 and AAR33280 represent the B. burgdorferi proteins P39-alpha and P39-beta. The DNA encodin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1993-017799/02.
N-PSDB; AAQ34672.
                                                                                                                                                                                                                                                                                                                                                                                   proteins was isolated by polymerase chain reaction (PCR) using primer sequences given in AAQ34673-76. This DNA contained two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 36-39; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAR-1990;
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374 YLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDKQ
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                                                                                                                                                                                                                                                                                                                                                                                        Local
                                 iigvdedgayl---apdnvitsttkdvgral----nift--snhlktntfeggk---li
                                                                                                    qyigsfadleagrsvatrmysdeid----
                                                                                                                                                                                                                                                                                                  gtfddksfnesalngvkkvkeefkielvlkesssnsylsdleg----lkdagsdliwlig 92
                                                                LIGYDTDQSLYYTKTKNKFFTSILKNLGYSYFSYLSDLYTKKSNSRNLAGFEFGKKSATV 373
                                                                                                                                  DKI----EINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANQ--NDRY 313
                                                                                                                                                                 gyiaakl-----sktgkigflggiegeivdafrygyeagakyan----kdikist 188
                                                                                                                                                                                                                                   fyrfsdvakvaalqnpdmkyai-----idpiysndpip-anlvgmtfraeegaflt 142
                                                                                                                                                                                                                                                                                                                                                                         85;
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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22.7%;
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                                                                                                                                                                                                                                                                                                                                                                     Score 165.5; DB 1
Pred. No. 0.00021;
0; Mismatches 134
                                                                                               -iihhaaglggigaievakelgsghy
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Search completed: July 18, 2002, 15:32:18 Job time: 185 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2002, 15:29:13; Search time 32.42 Seconds (without alignments)

Title: US-09-676-249A-2

Perfect score: 2299
Sequence: 1 MKKKIKWNKFLGLGLVFPLS......KQPDKQQESLDKLITDINKN 451

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138
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imum DB seq length: 0
imum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Listing first 45

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

			Result
25 26 27 28 29	16 17 18 20 21 22 23	1 2 2 3 3 4 4 4 7 7 7 7 11 11 11 11 11 11 11 11 11 11 1	No.
132 130 129.5 129.5 129.5 127.5	162 156.5 147 143.5 141.5 141.5 140.5 140.5	554.5 223 219 209 207 195.5 187.5 185.5 185.5 187.8 178 178 174 169.5 169.5	Score
5.55 5.7	5.000000000000000000000000000000000000	24. 9.1 9.5 9.5 17.9 17.9 17.4 17.4 17.4 17.4	Query Match
657 484 1140 1558 763	339 591 353 384 379 337 547	461 350 357 357 516 350 353 353 357 357 357 357 357	Length
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S73428 B90524 S73786 B71603 A82863	F70147 D64204 G70147 I40867 D82886 H75318 B97374 AH2591 E29504	B90555 G95097 G95097 G97965 F868064 D96986 C700946 C700418 F72418 E702418 E702418 E701417 AH1610 AH1	븅
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## ALIGNMENTS

ABC transporter xylose-binding lipoprotein [imported] - Mycoplasma pulmonis (strain U C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 03-Aug-2001
C;Accession: B90555
R;Chambaud, I.; Hellig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma p A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: B90555
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-461 < XUR>
A;Residues: 1-461 < XUR>
A;Cross-references: GB:AL445566; PID:g14089760; PIDN:CAC13519.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
C;Genetic:
A;Gene: MYPU\_3460
A;Genetic code: SGC3
Query Match

Query Match

24.1%; Score 554.5; DB 2; Length 461;
PID: GROSS DB 2;
PI

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conserved hypothetical protein spr0747 [imported] - Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001 C;Accession: C97965
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHc
                                                                                                                      RESULT
C97965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ilpoprotein [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;species: Streptococcus pneumoniae
C;bate: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: G95097
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heion, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison eference number: A95000; MUID:21357209; pMID:11463916
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A;Residues: 1-350 <KUR>
A;Cross-references: GB.AE005672; PIDN:AAK74976.1; PID:gl4972319; GSPDB:GN00164;
A;Experimental source: strain TIGR4
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                                                                                                                                                                                                                                                                                                        VSTLKQVGTTVKDI-----SNKAERGEFPGGQ---VIVYSLKDKGVDLAVTNLSEEG
                                                                                                                                                                                                                                                                                                                                        TSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATYYLGIKDRFVDIADTSLEGND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGG
                                                                                                                                                                                                                                         KKLATEAISEAKKEFEEKTKTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLIDDVIKDQKNV-----ASVTFADNESGYLAGVAAAK-----TTKTKQVGFVGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I-SPAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNKK----QWLGLGLV----AVAAVGLAACGNRSSRNAASSSDVKTK--------
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                                                                                                                                                                                                                    -AVEDAKAKILDGSVKVP
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1larity 24.8%; Pred. No. 1.7e-06;
Conservative 63; Mismatches 148;
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J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C. A;Title: Genome of the Bacterium Streptococcus pneumoniae A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: C97965
                                                      A; Molecule type: DNA
A; Residues: 1-350 <STO>
A; Cross-references: GB:
                                                                                                                                      A;Title: The complete genome sequence of the lactic acid A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: F86804
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A; Gene: spr0747
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A; Residues: 1-374 < KUR>
A; Cross-references: GB: AE007317;
                                     A; Experimental source:
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Best Local S
Matches 109
                  Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSTLKQVGTTVKDI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSSTAELE-----GKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                          KKLATEAISEAKKEFEEKTKTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- IVYQVAGGTGAGVFAEAKSLNESRPENEKVWVIGVDRDQEAEGKYTSKDGKESNFVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPSTLLAVAGPL-TEIFSDIIANQNDR-----YLIGVDTDQSL--VYT----KTKNKFF 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I-SPAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKD 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLIDDVIKDQKNV-----ASVTFADNESGYLAGVAAAK-----TTKTKQVGFVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FQSTSEADYANNLQQAAGSYNLI------FGVGFALHNAVEEVAKEHTDLNY 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109;
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                                                                                                                                                                                                                                                                                                                                                                                                           -AVEDAKAKILDGSVKVP
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                                     GB:AE005176; PID:g12724428; PIDN:AAK05536.1; GSPDB:GN00146
ce: strain IL1403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SNKAEKGEFPGGQ---VIVYSLKDKGVDLAVTNLSEEG
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; Pred. No. 3.3e-06;
62; Mismatches 150
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Strain R6
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Query Match

9

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Score

207;

B <u>ب</u>

Length

350;

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probable lipoprotein, Med/BMP family [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C; Accession: D96986 R; Nolling, J; Breton, G; Omelchenko, M,V; Markarova, X.S.; Zeng, Q.; Glbson, R; Nolling, J; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001
J. Bacteriol. 183, 4823-4838, 2001
J. Filtle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacter, R; Status: preliminary A, Scatus: preliminary A, Status: preliminary
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Best Local Similarity
Matches 100; Conserv
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Nesidues: 1-357 <KUR>
Cross-references: GB:AE001437; PIDN:AAK78679.1; PID:g15023581;
Experimental source: Clostridium acetobutylicum ATCC824
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Gene: CAC0702
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                                                     A-ELEGKYSSLANTNKNVWVLSGFQHGDAF-TRWLKIPENKQLFTE-----KNIIILG 171
                                                                                                               RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSST 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LATEAISEAKKEFEEKTKTIPAE 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLAVAGPL-TEIFSDIIA-----NQNDR-YLIGVDTDQSLV--YT----KTKNKFFTSIL
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                                                                                                                                                              IKKKT-----STTSSGSGNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VYQCAGGVGTGVFSEAKALNSTKNEADKVWVIGVDQDQEYLGKYKSKDGKDSNFVLVSTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VITRFEKGYEAGAKSVN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVIKDQKNV-----ASATFADNESAYLAGVAAAK-----ATKTNKIGFIGGMQSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKKR------VIAVSALALASVAVLAGCRSHDAAGSGK------
                  KDDYQPNLQSLIDNDSDLVFGVGYQMADDLATIAKKYPDKKFAIIDDAYDKQPKNI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEVG----NVVKDIADKTKDGKFPGGTIVTYDLKNGGVNLGL----DSANSEIK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVTOFTAGYLAGIKAWNLKNSDKKTKITTDKIEINLGEDVQDTSTKERLEQIASKDKPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDWIDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPIKRSAI-VIGGGISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YTYFQSNSASDYTTNYNSAEQQGYKLLFGTGFSLQDATSAAAK---NN---PKSNFVIVD
                                                                                                                                                                                                                                      Conservative
                                                                                         DTKK----VKVGLSTDEGGLNDKSFNQGADEGIKKAAKEYSVDYKAIESKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKTD-----LKAAIVTEIGGVNDRSFNQSAWEGL()SWGKENNLKKGTG
                                                                                                                                                                                                                                                   8.5%; Score 195.5; DB 2; 22.3%; Pred. No. 8.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.28;
                                                                                                                                                                                                                                 72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----PDIKVDVQYAGSFSDAAKGKTIAAAMYGAGDDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.7e-05;
2; Mismatches 156;
                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                    156;
                                                                                                                                                                                                                                   Indels 121;
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                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118;
                                                                                                                                                                                                                                                                                                                                                                                GSPDB:GN00168
                                                                                                                                                                                                                                   Gaps
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                                                                                       81
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                    137
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A;Genetic code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-516 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local (
                                 324 VYTKTKNKFFTSIL---KNLGYSVFSVLS--DLYTKKSNSRNLAGFEFGKKSATVYLGI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             329
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                                                                                                                                                                              227
                                                                                                                                                                                                                100 VYNNDNKAEFYKGADRVADVYFKVDEAAFLGGIAAAYMLNSNQAVFGAD----NKLTWGG
                                                                                                                                                                                                                                                                                                                      121 AE-LEGKYSSLANTNKNYWYLSGFQHGDAFTRWLKIPENKQ--LFTEK---NIILL---G
                                                                                                                                                                                                                                                                                                                                                             36
                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKKKIKWNKFLGLGLVFPLSAIATISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNE
                                                                                                                                                                           --GISPA-VTDFIAGYLAGIKAWNLKNSDKKTK---ITTDKIEINL------
                                                                                                                                                                                                                                      IDWIDTENVIPIG---RYINLTYKTEEAGWLAGYANASFLAKK---FPSDPIKRSAIVIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTVKDLVKGKK---
                                                                      SDSANAKKIIQELITKG-ADLILPVAIPQVGIAVTEAIATTSHNVGVIGVDVEIENDQAI
                                                                                                                                         YVGINAKNTTNYLAGFDLGVKWANEKLKDKNIKQEGTQETKKWINVEQVYASESSAGGFQ 215
                                                                                                                                                                                                                                                                                                                                                                                             RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNOSSWEAIQQLGALTGGEITSVDSST 120
                                                                                                                                                                                                                                                                                                                                                                                                                                  MKKLNKKVLFLAIGSVFALGTITVATSCTQKSTL-----
-- NKKTDKFINTHLSGNKN-GVIRFSITKRLDTATIKLLENAIKGESLSKKSDQIVIGSE
                                                                                                      VQDTSTKERLEQIASKDKPSTLLAVAGPLTEI-FSDIIANQNDRY-LIGVD----TDQSL
                                                                                                                                                                                                                                                                                     DEGFQTKYKSMASDGKRALLMPGYQH------PERLQNALVNDKFDPNLIALILDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGC3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 187.5; DB 2;
Pred. No. 0.00046;
7; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                           ----NYSQFYW--
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Length Indels

516;

Gaps

25;

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35 60

-TSPTSDD

49

171

-GFD

155

226 99

274

323

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A;Cross-references: GB:AE002100; GB:AF222894; NID:g6898946; PIDN:AAF30417.1; GSPDB:GN A;Experimental source: serovar 3; biovar 1
                                                                                                                                                           A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views A;Reference number: A82870 A;Accession: C82946
                                                                                                                                                                                                                                                           R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, submitted to GenBank, February 2000
                                                                                                                                                                                                                                                                                                                             hypothetical protein UU012 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_chang.C;Accession: C82946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLLAVAGPLTEIFSDIIANQNDR----YLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LINKFLSGYIAGAKTVN-----PNITVEK----NYTNDYSDTSKGKEVATSLYNGGCDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -MSLVFKEQEGSFLMG----VIAGKM----TKTNKIGFVGGKDQP
                                                                                                                                                                                                                                                                                                                                                               20-Aug-2000 #text_change 20-Aug-2000
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C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: C70009
C:Accession: C70009
R:Kunst, F.; Ogasawara, N.; Moszer, T.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
R:Kunst, F.; Ogasawara, N.; Moszer, T.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
R:Kunst, F.; Ogasawara, N.; Moszer, T.; Albertini, K.D.; Capuano, V.; Carter, N.M.; Chc
Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

ure 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galier
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rleger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakas, T.; Tanaka, T.; Togsto, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Reference number: A69580; MUID:98044033
A; Accession: C70009
A; Status, Togaliminary: nucleic and sequence of the Gram-positive bacterium Bacillus subtilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   est Local Similarity
atches 106; Conserv
                                                                                                                                                                          187
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AIVTAGGTVNDNSFNQSSWEAIQQLGALTG-----GEITSVDSSTAELEGKYSSLANTN 134
                                                                         KKEDPKRDVWVIGVDKDQYAEGQVEGTDDNVTLTSMVK----KVDTVVEDV-TKKASDGK 291
                                                                                                                                                                                                                                                                                                                                                                                                                    KNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGID-WTDTENVIPTGRYINLTYKT 193
                                                                                                                                                                          ----AVVEVKYAGGFDKADVGKATAESM----YKSGVDVIYHSAGATGTGVFTE-AKNL
                                                                                                                                                                                                                     KKTKITTDKIEINLGFDVQDT--STKERLEQIASKDKPSTLLAVAGPL-TEIFSDIIAN-
                                                                                                                                                                                                                                                                        QEGSFLVGVAAAL-----SSKSGKIGFVGGMESELIKKFEVGFRAGVQAVNPK---
                                                                                                                                                                                                                                                                                                                        EEAGWLAGYANASFLAKKFPSDPTKRSAI-VIGGGISPAVTDFIAGYLAGIKAWNLKNSD
                                                                                                                                                                                                                                                                                                                                                                      FDLIYGVGYLMEDSIS---EIADQR-----KNTNFAIIDAVVDKDNV-----ASITFKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGTILGACGNSE--KSSGSGEGKNK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVRKTLEIPEMPDKQPDKQQES 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMVTDVGGVDDKSFNQSAWEGIQAFGKENGLKKGKNGYDYLQSKSDADYTTNLNKLAREN
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                                                                                                                       -QNDRYLIGVDTDQ----SLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABC transporter
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168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 185.5; DB 1;
Pred. No. 0.00035;
1; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence
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A; Accession: A43595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-353 <COL>
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Best Local
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                                                                         365
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                                                                                                                                                                                                                        194
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                                                                                                                                                                                                                                                    TKITTDKIEINLGFDVQDT-STKERLEQIASK---DKPSTLLAVAG----PLTEIFSDII 306
                                                                                                                                                                     ANQNDRYLIGVDTDQSL--VYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGF 364
                                                                                                                                                                                                                                                                                                                                                                                                                    VACGSFLVEA-----VIETSARFPKQKFLVIDAVVQDRDNV-----VSAVFGQNEGSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGMVTDSGDIDDKSFNQQVWEGISRFAQENNAKCKYVTASTDAEYVPSLSAFADENMGLV 101
                                                                       EFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTL 424
                                                                                                                                                                                                                                                                                                                      LVGVA-AALKAKE----AGKSAVGFIVGMELGMMPL---FEAGFEAGVKAVD-----
                                                                                                                                                                                                                                                                                                                                                                    LAGYANASFLAKKFPSDPTKRSAI - - VIGG - - GISPAVTDFIAGYLAGIKAWNLKNSDKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGW 198
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                                                                                                                          LNGQDVWVIGVDRDQYMDGVYDGSKSVVLTSMVKRA-----DVAAERISKMAYDGSFPG-
                                                                                                                                                                                                                        -----PDIQVVVEVANTFSDPQKGQALAAKLYDSGVNVIFQVAGGTGNGVIKEARDRR
                         -GQSIMFGLEDKAVGIPE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Indels

74;

Gaps

17;

254 149

193

-ENPNLSSAVMEKIRSFEEKI---

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C;Keywords: blocked amino end; lipoprotein; membrane protein; thiolester F;1-20/Domain: signal sequence #status predicted <SIG> F;21-353/product; membrane lipoprotein tmpC #status predicted <MAT> F;21/Modified site: fatty acylated amino end (Cys) (in mature form) #status F;21/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-10,'A',12-158,'R',160-353 <SCH>
A;Cross-references: GB:X57836; NID:948838; PINN:CAA40968.1;
A;Note: this protein is shown to incorporate palmitic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis A;Reference number: A71250; MUID:98332770
A;Accession: H71340
                                                                                                                                                                                                                                                                                                                                         A;Start codon: GTG
C;Superfamily: ABC transporter yufN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Schouls, L.R., va., 336-3546, 1991
Infect. Immun. 59, 3356-3546, 1991
A;Title: Characterization of the 35-kilodalton Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE001211; GB:AE000520; NID:g3322582; A;Experimental source: strain Nichols R;Schouls, L.M.; van der Heide, H.G.J.; van Embden, J.D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane lipoprotein TmpC precursor - syphilis spirochete C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Species: 07-Aug-1998 #sequence_revision 07-Aug-1998 #text_change 23-Jul-1999 C;Accession: H71340; A43595; S29561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not shown;
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                                   7.98;
23.78;
; Score 182; DB 1; L; Pred. No. 0.00058; 69; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation
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                                                                   Length
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Utterback,
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C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: F72418
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hid
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Richardson,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                            basic membrane lipoprotein B (bmpB) - Lyme disease spirochete C. Species: Borrelia burgdorferi (Lyme disease spirochete) C. Species: Borrelia burgdorferi (Lyme disease spirochete) C. Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 29-Sep-1999 C. Accession: E70147; I40290; I40242 N.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatking 1997 Nature 390, 580-586, 1997
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Nature 390, 580-58
A; Authors: Smith,
A; Title: Genomic s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  basic membrane protein - Thermotoga maritima (strain MSB8)
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Best Local S
Matches 94
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                                                                                                                                                                                                                                                      323
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                                                                                                                                                                                                                                                                                                                                                                                                                     --ASKDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNL
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                                                                                                                                                                                                                                                     IAELLYLEKLMKEGTLKVPETQEELDAFEVPQI
                                                                                                                                                                                                                                                                                        ISE---AKKEFEEKTKTIP-AEEVRKTLEIPEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYEAGIKTYSVLHK-KNVKILRGYTQDFEDPKKGKDLAMSQFAEGADIVFHASGACGNGV
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sequence
                    H.O.;
                    Venter,
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 of a
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                  J.C.
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Pred. No. 0.00064;
disease
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 spirochaete,
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burgdorferi
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                                                                   Vugt,
                                                                                        Whit
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R;Ojaimi, C.; Davidson, B.E.; Saint Girons Microbiology 140, 2931-2940, 1994
A;Title: Conservation of gene arrangement A;Reference number: I40241; MUID:95111614
A;Accession: I40242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; MoLecule type: DNA, A; A6-179 <RE2> A; Residues: 1-44, 'A', 46-179 <RE2> A; Cross-references: GB:L35050; NID:9516591; C; Superfamily: basic membrane protein C
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A; Residues: 1-232, 'A', 234-317, 'V', 319-341 < E
A; Cross-references: GB:L24194; NID:9508420;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Simpson, W.J.; Cieplak, W. FEMS Microbiol. Lett. 119, 3
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A;Experimental source: strain B31
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A; Residues: 1-341 <KLE>
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Accession: E70147
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KVLERKIINKEIIVP
                                                                   IKNNNV-----WEGGK----VVQMGLRDGVIGLPNAN
                                                                                                                                              AAGLAGIGVIETAKNLGDGYYVIGADQDQS--YLAPKN-FITSVIKNIGDALYLITGE-Y
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I.; Old, I.G.
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C;Becies: Listeria innocua
C;Becies: Listeria innocua
C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #tex
C;Accession: AH1610
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; CD4+ T cell-stimulating antigen, lipoprotein [imported] - Listeria #text\_change 27 innocua

(strain

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Science 294, D.; Jones, Dominguez-Bernal, G.; Jones, L.M.; Karst, )4, 849-852, : : Kreft, J.; ! 2001 Dussurget, Baquero, F surget, O.; F.; Berch; Entian, Berche, ; Bloec Fsihi,

A; Authors: ok, C.; Scl Schlueter, Kuhn, M.; ; Simoes, 1 , Kunst, F.; N.; Tierrez, Kurapkat, G.; Madueno,
, A.; Vazquez-Boland, J . P. ; Maitournam, A.; Voss, H.; Wehla

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A;Accessau. A;Accessau. A;Accessau. A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <GLA>
A;Cross-references: GB;AL592022; pIDN:CAC96656.1;
A;Cross-references: strain Clip11262
                                                                                                               A; Molecule type: DNA
A; Residues: 1-360 <KLE>
A; Cross-references: GB:AE001144; GB:AE000783;
A; Experimental source: strain B31
C; Superfamily: basic membrane protein C
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                                                                                                                                                                                                    Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease
A;Reference number: A70100; MUID:98065943
A;Accession: H70147
                                                                                                                                                                                                                                                           R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
                                                                                                                                                                                                                                                                                                                    C:Species: Borrelia burgdorferi (Lyme disease spirochete C:Species: Borrelia burgdorferi (Lyme disease spirochete) C:Date: 11-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 29-Sep-1999 C:Accession: H70147
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                                            Query Ma
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VYLGIKDREVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMP
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                                                           Similarity
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                                           64;
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                                         Score 169.5; DB Pred. No. 0.0035; 4; Mismatches 1:
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                                                                      DB 2;
                                           137;
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A;Rctessau...
A;Status; preliminary
A;Molecule type: DNA
A;Residues: 1-357 <GLA>
A;Cross-references: GB:MC_003210; PIDN:CAC99466.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; E.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.
A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AD1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AD1248
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                                                                                                                                                                                     KVGFVGGVKGTVIDRFEAGFTAGVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                     GGEITSVDSSTAELEGKYSSLANTNKNVWVLS-----GFQHGDAFTRWLK-IPENKQ 160
-SLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAG-FEFGKKSATVYLGIKD : | | | | | | | | : | : |:
                                                                                                                              ERLEQIASKDKPS----TLLAVAGPLTEIFSDIIANQNDR-----YLIGVDTDQ-----
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                                                                                                                                                                                                                                                                                                                                                                                      GTDGYNYLQSASEADYK-----TNLNTAVRSDYDLIYGIGYKLKDAIEEVSKQKPKNQF 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKYSSLANTNKN-VWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPT 183
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Pred. No. 0.0037;
3; Mismatches 14
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urget, O.; Entian,
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Voss, H.; Wehla
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K.D.; F
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
hypothetical membrane C; Species: Ureaplasma
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Best Local :
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Residues: 1-525 <GLA>
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Xper1mental source: serovar 3; biovar 1
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                                                                                                                                                                                                                                                                  ANGKTIIFSIVKRLDLAFKGALLKASEGAQLINDINKDAYKLGTHT!:ASF--NKNTYVD-
                                                                                                                                                                                                                                                                                                      KNLGYSVFSVLS--DLYTK-----KSNSRNLAGFEFGKKSATVYLGIKDRFVDI 384
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                                                                                                                                                     KTIPAEEVRKTLEIPEMP---
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                                                                                                                                                                                         -NTALVELSKAGHQYLIDAIKLSGLKEVNDYKTIVEIIQEDPLFKLLSQIGTKKLDEVAT
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lipoprotein UU016 [imported] - Ureaplasma urealyticum urealyticum
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A;Molecule type: DNA
A;Residues: 1-524 <GLA>
A;Cross-references: GB:AE002101; GB:AF222894; NID:g6898957; PIDN:AAF30421.1; GSPDB:GN
A;Experimental source: serovar 3; biovar 1
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A; Accession: D82944
A; Status: preliminary
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C;Accession: D82944
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.;
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                                KTKTIPAEEVRKTLEIPEMPDKQPDKQQESLDKLI 445
                                                                                                                                                                            -----VYTKTKNKFFT----SILKNLGYSVFSVLSDLY--TKKSNSRNLAGFEFGKKSAT
                                                                                                                                                                                                                                                                                                                          DFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKER----LEQI-ASK---
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                                                                    SL----DKSTYVDDTPLVELSNAGRVYLEQAAKLAGLKAITYAQIVNVIQNEELFKLLST
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                                                                                                                                                                                                                                                    TFIQGFKLGVQWANEKLKDK-----EIN----QEDANGSKKKWMNVEQVFASKYVA
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Search completed: July 18, 2002, 15:29:55 Job time: 42 sec

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MERA_STAAU
Y040_MYCPN
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FLGK_SALTY
LBPA_NEIMB
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005252;

15-DEC-1998 (Rel. 37, Created)

15-DEC-1998 (Rel. 37, Last sequence upda

16-OCT-2001 (Rel. 40, Last annotation up

Hypothetical lipoprotein yufN precursor.
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Result No.

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Database

## ALIGNMENTS

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Bacillus Subtilis. Bacillus/Staphylococcus group: Bacillus/Clostridium group; Bacillus/Staphylococcus group: Bacillus. NCBL TaxID-1423; [1] SEQUENCE FROM N.A. STRAIN-168; Oudega B., Koningsteyn G., Duesterhoeft A., Hilbert H.; SUBCELLULAR LOCATION: Attached to the membrane by a lipid (Fotential). (Fotential). SIMILENTY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioliformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entitles requires a license agreement (See http://www.isb-sib or send an email to license eds remember of the swiss institutions as long as its content is motified and this statement is not removed. Usage by and for send an email to license eds remember of the swiss institute. There are no restrict use by non-profit institutions as long as its content is motified and this statement is not removed. Usage by and for send an email to license eds remember (See http://www.isb-sib or send an email to license eds remember (See http://www.isb-sib or send an email to license eds remember (See http://www.isb-sib or send an email to license eds remember (See http://www.isb-sib or send an email to license eds remember (See http://www.isb-sib or send an email to license eds remember (See http://www.isb-sib or send an email to license eds remember (See http://www.isb-sib or send an email to license eds remember (See http://www.isb-sib or send an email to license eds remember (See http://www.isb-sib or send an email to license eds remember (See http://www.isb-sib or send an email to license eds remember (See http://www.isb-sib or send an email to license eds remember (See http://www.isb-sib or send an email to license eds remember (See http://www.isb-sib or send an email to license eds remember (See http://www.isb-sib or send an email to license eds remember (See http://www
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031357; 031360;
15-DEC-1998 (Rel. 37, C
15-DEC-1998 (Rel. 37, L
15-DEC-1998 (Rel. 37, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Clin. Microbic
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                                                                       SIGNAL
                                                                                                                        Antigen;
                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                   LIPID
                                                                                                                                                                      Pfam; PF02608; Bmp; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roessler D., Hauser U., Wilske B.; "Heterogeneity of BmpA (P39) among European burgdorferi seasu lato and influence of inte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia garinii.
Bacteria; Spirochaetales;
NCBI_TaxID=29519;
                                                                                                                                                                                                                    InterPro; IPR003760; Bmp.
InterPro; IPR000437; Prok_lipoprot.
                                                                                                                                                                                                                                                                          EMBL; X97244; CAA65883.1; -. EMBL; X97238; CAA65877.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
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MEDLINE-98010210; PubMed-9350727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clin. Microbiol. 35:2752-2758(1997).
FUNCTION: NOT KNOWN; IMMUNOGENIC PROTEIN.
SUBCELLULAR LOCATION: Attached to the membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS.
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n A precursor (Immunodominant antigen
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G -> D (IN STRAIN PLI).
S -> N (IN STRAIN PLI).
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Matches 93
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P29724; O83339;
O1-APR-1993 (Rel. 25, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Membrane lipoprotein tmpC precursor (Membrane
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                       Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G. Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterbac McDonald L., Artlach P., Bowman C., Cotton M.D., Fujii C., Garl Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith
                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-NICHOLS; MEDLINE-98332770;
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STRAIN-NICHOLS;
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Bacteria; Spirochaetales;
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 STANDARD; PRT; 34
; O31317; O50168; Q44858;
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MEDLINB-98065943; PubMed-9403685;

Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.P.

Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K.,

Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,

Peterson J., Kerlavage A.R., Quackenbush J., Saizberg S., Har

van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Meidman J.,

Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,

Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatc
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STRAIN-ATCC 35210 / B31;

MEDLINE-9801.0210; PubMed-9350727;

Roessler D., Hauser U., Wilske B.;

"Heterogeneity of EmpA (P39) among European isolates burgdorferi sensu lato and influence of interspecies serodiagnosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94327086; PubMed-8050720; Simpson W.J., Cieplak W., Schrumpf M.E., "Nucleotide sequence and analysis of the encoding the immunogenic P39 antigen."; FEMS Microbiol. Lett. 119:381-388(1994).
                                                                                                                                                                                                                                                                                                                                                                                                      "Conservation of gene arrangement and an unusual organization of genes in the linear chromosomes of the Lyme disease spirochaetes Borrelia burgdorferi, B. garinii and B. afzelii.";
Microbiology 140:2931-2940(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97132632; PubMed-8978084;
Aron L., Toth C., Godfrey H.P., Cabello F.C.;
"Identification and mapping of a chromosomal oburgdorferi containing genes expressed in vive FEMS Microbiol. Lett. 145:309-314(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genomic sequence of a Lyme burgdorferi ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Garland S., Fujii C., Smith H.O., Venter J
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; X81517; CAA57237.1; -. 

; AE001143; AAC66758.1; -. 

; L35050; AAC41402.1; -. 

; BB0382; -.
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                                                            L24194; AAA72407.1;
U49938; AAC44713.1;
X81517; CAA57237.1;
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Best Local Similarity
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SEQUENCE FROM N.A.

STRAIN-CLIP 11262 / Serovar 6a;

STRAIN-CLIP 11262 / Serovar 6a;

STRAIN-CLIP 11262 / Serovar 6a;

MEDLINE-21537279; PubMed-11679669;

Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Charbit A., Chetouani F., Couve E., de Durvar L., Dussurget C.

Charbit A., Chetouani F., Couve E., de Daruvar L., Dussurget C.

Charbit A., Chetouani F., Couve E., de Daruvar L., Dussurget C.

Charbit A., Chetouani F., Couve E., de Daruvar L., Dussurget C.

Charbit A., Fishi H., Garcia-del Portillo F., Garrido P.,

Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson I.

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Mata Vicente J., Ng E., Nedjari H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
CONFLICT
SEQUENCE
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01-MAR-2002 (Rel. 41,
01-MAR-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PFC
PROSITE;
                                                                                                                                                                                                                                                                                                        Listeria innocua.
Bacteria; Firmicutes; Bacteria; Firmicutes; Bacillus/Staphylococcus
Bacillus/Staphylococcus
CBI_TaxID=1642;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rPro; IPR003760;
PF02608; Bmp; 1
[TE; PS00013; PRO]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KTIPAEEVRKTLEIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGPLIEI-FSDIIANQND-RYLIGVDIDQSLVYTKIKNKFFISILKNLGYSVFSVLSDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YGYESGAKYAN-KDIEIISEYSNSFSDVDIG------RTIASKWYSKGIDVIHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASK--DKPSTLLAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --LANTNKN-----VWVLSGFQHGDAFTRWLKIPENKQLFTEKNII--ILGIDWTDTENVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSKKIKISMLV---DGVLDDKSFNSSANEALLRLKKDFPENIEEVFS--CAISGVYSSYV
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13; PROKAR_LIPOPROTEIN;
Comple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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Last annotation updat
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Pred. No. 0.000
59; Mismatches
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-> A (IN STRAIN 212).

-> T (IN STRAIN B31).

-> I (IN STRAIN B31).

-> P (IN REF. 3).

-> P (IN REF. 3).
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Best Local
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15-DEC-1998
15-DEC-1998
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SEQUENCE
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SIGNAL
CHAIN
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the Euro
        Borrelia garinii.
Bacteria; Spirochaetales;
NCBI_TaxID=29519;
                                                  BMPB
                                                                                                                                           BORGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Remmel B., Rose M., Schlueter T., Simoes N.,
Vazquez-Boland J.-A., Voss H., Wehland J., C.
"Comparative genomics of Listeria species.";
Science 294:849-852(2001).
                                                              Basic
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Buropean Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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                                                                                                                                                                                                                    VYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMP
                                                                                                                                                                                                                                                                                                ANDFAKADKGQQIASSMYSSGVDVIFHAAGGTGNGVFAE-AKNLKKKDPSRAVWVIGVDR
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sen the Swiss Institute of Bioinformatics
                                                                                                                                                                                          IEYGLDKDAVGLSE-----HQDNISKDVLAKVE---EYKQKIVDGD---
                                                                                                                                                                                                                                                                                                                                                   --TTKTNKVGFVGGVKGAVIDRFEAGFTAGVKA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALT----GGEITSVDSSTAELEGKYSSLANTNKNVWVLS------GFQHGDAFTRWLK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGVVLGACGSSSDDKKS-----GDDKSSKDFTVAMVTDTGGVDDRSFNQSAWEGLQKFG
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1 22 PROBABLE.
23 357 CD4+ T CELI
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357
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                                                            protein
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37,
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38357 MW;
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Last annotation update)
n B precursor.
                                                                                                    Created)
                        Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 174; DB
Pred. No. 0.000
62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD4+ T CELL-STIMULATING N-ACYL DIGLYCERIDE (PROE; 2EDA2AA9820A3FBC CRC64
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Best Local 9
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Q447/43;
15-DEC-1998 (Rel. 37, C
15-DEC-1998 (Rel. 37, L
16-OCT-2001 (Rel. 40, L
Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; S NCBI_TaxID=139; [1]
                                                   Basic membrane protein BMPD OR BB0385.
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J. Clin. Microbiol. 35:2752-2758(1997).
Attached to the membrane
                                                                                                                                              BORBU
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SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS
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                                                                                                                                                                                                                                                                          D----RYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEF
                                                                                                                                                                                                GK---IIQMGLRDGVVGLSNANKFEYIKVIERKIVNEEI
                                                                                                                                                                                                                         GKKSATVYLGIKDRFVDIADTS----LEGNDKKLATEAI 401
                                                                                                                                                                                                                                                   ELGDGYYVIGADQDQSHL---APRNFITSVIKNVGDALYLVTSE-YLKNNNT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF02608; Bmp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X81518; CAA57238.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lipoprotein; Signal.
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ty of BmpA (P39) among European isolates
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                                                                                                                                STANDARD;
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341
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37236
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                                                                                                       Created)
                                                                D precursor
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                           Spirochaetaceae; Borrelia
                                       disease
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N-ACYL DIGLYCERIDE (PRO
; 442BEF0BFEDDOC9A CRC6
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Pred. No. 0.
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                                       spirochete)
                                                                                          update)
                                                                                                                                341
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                                                                            update)
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CRC64;
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STRAIN-ARCC 35210 / B31;

MEDLINE-98065943; PubMed-9403685;

MEDLINE-98065943; PubMed-9403685;

Lathigra R., White O., Retchum K.A., Dodson R., Hickey E.K.

Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,

Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S.,

Peterson J., Kerlavage A.R., Goagne J.D., Weidman

Utterback T., Watthey L., McDonald L., Artiach P., Bowman

Garland S., Fujii C., Cotton M.D., Horst K., Roberts K.,

Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
CHAIN
LIPID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-slb.or send an email to license@isb-slb.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ramamoorthy R., Povinelli L., Philipp M.T.; Molecular characterization, genomic arrangement, and SmpD, a new member of the bmp class of genes encoding proteins of Borrelia burgdorferi."; Infect. Immun. 64:1259-1264(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genomic sequence of a Lyme disease spirochaete,
burgdorferi.";
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PROSITE; PS00013; PROKAR_LIPOPROTEIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96178617; PubMed=8606088;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
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                                                                                                                                                                                                                                                                                                                                     Match
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 NSRNLAGFEFGKKSATVYLGIK-DRFVDIADTSLEGNDKKLATEAI
                                            TEIFSDIIANQ--NDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKS
                                                                                                            IKAWNLKNSDKKTKITTDKI----EINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPL
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                           SGIGVIEAAKELGPDHYIIGVDQDQSYL---APNNVIVSAVKKVDSLMYSL-
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                                                                                                                                                                                                                                                                                                                                                                                                                  Lipoprotein; Signal; Complete proteome 1 16 PROBABLE.
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                                                                                                                                                                                                                                                                                                                                                                            341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144; AAB91505.1;
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                  -SNIKVVSQYVGTFGDFGLG----RSTASNM----YRDGVDIIFAAAG-L
                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                           341
17
                                                                                                                                                                                                                                                                                                                                                                              37163 MW;
                                                                                                                                                                                                                                                                                                                     7.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TO THE BMP FAMILY OF LIPOPROTEINS
                                                                                                                                                                                                                                                                                                          64;
                                                                                                                                                                                                                                                                                                                    Score 169.5; DE Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                           BASIC MEMBRANE PROTEIN D.
N-ACYL DIGLYCERIDE (PROBABLE)
; 63FF6638F81A91D5 CRC64;
                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane
                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borrelia
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                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                    Length
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  401
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                                                                                                                                                                                                                                                                                                        57;
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                                                            Query Match
Best Local S
Matches 98
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Q48754;
15-DEC-1998 (Rel. 37, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
CD4+ T cell-stimulating antigen precursor.
                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baguero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn T., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Sinces N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
Science 294:849-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-EGD-e / Serovar 1/2a;
MEDLINE-21537279; Pubmed-11679669;
                                                                                                                                                                                                                                                                                                                                                         EMBL; AL591979; CAC99466.1; -
EMBL; S80336; AAB35725.2; ALT_TERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *Sanderson S., Campbell D.J., Shastri N.;
"Identification of a CD4+ T cell-stimulating antigen bacteria by expression cloning.";
J. Exp. Med. 182:1751-1757(1995).
                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-252 FROM N.A. STRAIN-85EO-1167;
                                                                                                                                                                                                                                                                                                                ListiList; LMO01388; -.
InterPro; IPR003760; Bmp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96096448; PubMed=7500019;
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NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group;
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                   54 ISGLVNERKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Probable).
SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Attached to the membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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                                                              98; Conservative
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357
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38415
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                                                                                                                                                                      ME:
                                                                63;
                                                            Score 169; DB
Pred. No. 0.003
53; Mismatches
                                                                                                                                                                 N-ACYL DIGLYCERIDE (PROBABLE). 83605B8B6419C8D1 CRC64;
                                                                                                                                                                                                          CD4+ T CELL-STIMULATING ANTIGEN
Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357
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                                                                               DB 1;
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                                                              144;
                                                                                                   Length 357;
                                                              Indels 106;
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RESULT 9
BMPA_BORAF
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                            CHAIN
LIPID
                                                                                                                                                                                                    EMBL; X81516; CAA57236.1; -. EMBL; X97237; CAA65876.1; -. EMBL; X97239; CAA65878.1; -. EMBL; X97241; CAA65880.1; -.
                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Heterogeneity of BmpA (P39) among European isolates burgdorferi sensu lato and influence of interspecies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98010210; PubMed-9350727;
Roessler D., Hauser U., Wilske B.;
"Heterogeneity of BmpA (P39) among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia afzelii.
Bacteria; Spiroch
     VARIANT
                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>'</del>-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    serodiagnosis."
J. Clin. Microb
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                                                                                                    Antigen;
                                                                                                                            PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=29518;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Probable). SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clin. Microbiol. 35:2752-2758(1997).
FUNCTION: NOT KNOWN; IMMUNOGENIC PROTEIN
SUBCELLULAR LOCATION: Attached to the mer
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2; PS00013; PROKAR_LIPOPROTEIN; 1.

1; Membrane; Lipoprotein; Signal.

1 17

1 19 PROBABLE.

1 8 39 BASIC MEMBRA

1 18 N-ACYL DIGLY

1 125 125 A -> S (IN S
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                                                                                                                                                      Bmp;
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PROBABLE.

BASIC MEMBRANE PROTEIN A.

N-ACYL DIGLYCERIDE (PROBA

A -> S (IN STRAIN PLE).
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variability
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Aron L., Toth C., Godfrey H.P., Cabello F.C.;
"Identification and mapping of a chromosomal burgdorferi containing genes expressed in viv
FEMS Microbiol. Lett. 145:309-314(1996).
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STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
Fraser C.M., Casjens S., Huang W.M.,
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-i- FUNCTION: NOT KNOWN; IMMUNOGENIC PROTEIN.
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the European Bioinformatics Institute
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Pred. No. 0.
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N-ACYL DIGLYCERIDE (PROBABLE).
F -> S (IN STRAIN 297).
A9581868CA7DB923 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 448-517 FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE-94075230; PubMed-8253680;
Peterson S.M., Hu P.-C., Bott K.F., Hutchison
Peterson S.M., Hu P.-C., Bott K.F., Hutchison
Peterson S.M., Hu P.-C., Bott K.F., Hutchison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-ATCC 33530 / G-37;

MEDLINE-96026346; PubMed-7569993;

Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Myuyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Peterson S. M., Smalth H.O., Hutchson C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403(1995).
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01-OCT-1996
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U39683; AAC71256.1;
EMBL; U02125; AAD12400.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quencing.;
Bacteriol. 175:7918-7930(1993).
- SUBCELLULAR LOCATION: Attached
ANKHFGLNMAIVTAG--GTVNDNSFNQSSWEAIQQLGALTGG-EITSVDSSTAELEGK--
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                                                                84;
                                                            Score 156.5; I
Pred. No. 0.01
B4; Mismatches
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N-ACYL DIGLYCERIDE (POTENTIAL);
14A8FA31BB7E0928 CRC64;
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                                          Membrane;
SIGNAL
                                                                                 Pfam; PF02608; Bmp;
                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                     MEDLINE-98010210; PubMed-9350727;
Roessler D., Hauser U., Wilske B.;
"Heterogeneity of BmpA (P39) among European isolates
burgdorferi sensu lato and influence of interspecies
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15-DEC-1998 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FL-----AKKFPSDPTKRSAIVIGG--GIS-PAVTDFIAGYLAGIKAWN-----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKNNSVGVSEAGYEFLIDPVFWKNTSSMQAMSLSASLKANAASSSDNKKKLSEVATK 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKDREVDIADT -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKDKLKMGNKKIIPFSSI-KALDVAVESILSTL--EKGSSQN--GYQGFGYNN----IGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPRAITIANNLIDKGVNAIIPIAGPQTNLVVTQIARRQAHTAVIGVDSAQELLDINIDAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KERLEQIASK--DK-PSTLLAVAGPLTE-IFSDIIANQNDRYLIGVDTDQSL----VYTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDAQDSSAQVTTSKQTVLKQLQVANGEKRIKKIKWISPKQGSDGETINIQDHQSGSFSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNS-DKKTKITTDK-----IEINLG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DWIDTENVIPIG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -QSDKESLAKTGFIFVDGAIEKEFNKRNGVPQFKSTPTNISSVAFRSDDGSFLTGVATAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WKRPGFTLSDRIATFNNIKNDGSDVIVATGFNQ------QESLQAITSDDIRF---
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                                                                    PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                           Microbiol. 35:2752-2758(1997).
                                        Lipoprotein; Signal
                                                                                               IPR003760;
 Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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37,
341
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37198
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                                                                                             Bmp.
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Last annotation
n B precursor.
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 MW.
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BASIC MEMBRANE PROTEIN
N-ACYL DIGLYCERIDE (PRO
; 1E8EA3E3D54ACDB1 CRC6
                                           PROBABLE
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CRC64;
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variability
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BMPC_BORBU STANDARD,
050169; Q44859;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
  Smith H.O
         Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton Lathigra R., White O., KetChum K.A., Dodson R., Hickey E.K. Dougherty B., Tomb J.-F., Fleischmann R.D., Richardison D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman Utterback T., Watthey L., McDonald L., Artiach P., Bowman Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                   Aron L., Alekshun Cabello F.;
                                                                                                                  SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
                                                                                                                                                                       Aron L., Toth C., Godfrey H.P., Cabello F.C.; "Identification and mapping of a chromosomal geburgdorferi containing genes expressed in vivo. FEMS Microbiol. Lett. 145:309-314(1996).
                                                                                                                                                                                                                                                                             "Cloning and DNA sequence analysis of bmpC, a gene encodi potential membrane lipoprotein of Borrelia burgdorferi."; FEMS Microbiol. Lett. 123:75-82(1994).
                                                                                                                                                                                                                                                                                                                                                                                                              Borrelia burgdorferi (Lyme
Bacteria; Spirochaetales; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BORBU
                                                                                                                                                                                                                          MEDLINE=97132632; PubMed=8978084;
                                                                                                                                                                                                                                                                                                                                               MEDLINE=95080623;
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAFLAGY - - - - IAAKKSVS - - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLSGFQHGD-AFTRWLKIPENKQLFTEKNII--ILGIDWTDTENVIPTGRYINLTYKTEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVLDDKSFNSSANEALLRLKKDFPENIEKVFSSA--VSGVYSSYVSDLDNLKMNGSGLIW 93
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Lyme
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Spirochaetaceae; Borrelia
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disease
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                                                                                                                                                                                                                                                                                                                                Schwartz I.,
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No. 0.
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on update)
spirochaete,
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                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                              Godfrey H.P.,
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                                                                                                       Clayton R.A.,
                                                                                                                                                                                                cluster
                                                                            D.,
                          Hatch
                                                                 Hanson
                                                                                                                                                                                                 of Borrelia
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                                                                                          Gwinn M.,
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                                                                                                                                                                                     RESULT
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SEQUENCE
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Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
                                                            Streptococcus pyogenes. Bacteria; Firmicutes; F
                                                                                               16-OCT-2001 (Rel. 40, Last
16-OCT-2001 (Rel. 40, Last
Probable dipeptidase B (EC
                                                                                                                                    Q99XS1;
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Attached to the membrane by a 1: (Probable).
-!- SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS
STRAIN=SF3.70 / ATCC 700294 / Serotype
            SEQUENCE FROM N.A.
                                    NCBI_TaxID=1314;
                                                Streptococcus
                                                                                     PEPDB OR SPY2066.
                                                                                                                                                              PEDB_STRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02608; Bmp; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
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                                                                                                                                                                                                                        289 ---NNRVFKG-----GITIDRGLKEGVIEIVKDPDVLNN--RLVDEVIDLENK
                                                                                                                                                                                                                                                                                                                                                                                                                                                 128
                                                                                                                                                                                                                                                                                                                                                                                                                         92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 VTAGGTVNDNSFNQSSWEAIQQLG------ALTGGEITSVDSSTAELEGKY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIG---GGISPAVTDFIAGYL
                                                                                                                                                                                                                                                                                                                                                                                                                                               SSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGI----DWTDTENVIPT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLAHGSFYDKGYNQSVHDGVVKLRDNFGIKLITKSLRPYPIEGKRLLTVDE--AMTEDAY
                                                                                                                                                                                                                                               KKSNSRNLAGFEFGKKSATVYLGIKDRFVDIA-DTSLEGNDKKLATEAISEAKK
                                                                                                                                                                                                                                                                                                                         AGIFYANPKLRLVSKKAPSLFD
                                                                                                                                                                                                                                                                                                                                                AGIKAWN--LKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIA----
                                                                                                                                                                                                                                                                                                                                                                          NS-LAIKFRNEEAAFLAGYIAAKMSRKE----
                                                                                                                                                                                                                                                                                                                                                                                                                         EVQKNPLNLFWLI-GYRFSDL-----SVKLSYERPDIYYGIIDAFDYGDIQ--VPK
                                                                                                                                                                                                                                                                        AGITGLGVYDAAKELGPKYYVIGLNQDQSYI---APQNVITSIIKDIGKVIYSISSEYI-
                                                                                                                                                                                                                                                                                              AGPLTEIFSDIIANQNDR-YLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR003760;
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353
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179 V
179 V
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23.7%;
                                                             Bacillus/Clostridium
                                                                                               t sequence up t annotation 3.4.-.-).
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V -> L (IN STRAIN 297).
; 2E8FF607D6CAB9B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 147;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASIC MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROBABLE.
                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                         npdate)
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M1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There are no restrictions
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-i- CATALYTIC ACTIVITY: DIPEPTIDE + H(2)0 - 2 AMINO ACID.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY U34.
SCA4_RICFE ST/
Q9AJ37;
16-OCT-2001 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDNPAGEKWKDLSNGFEYPLPEHSYRYSAIPDVTPNKGVYDE------AGFNE-FGV 112
                                                                                                                                                                    ITD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTGRYINLTYKTEEAGWLAGYANASFLAKKF--PSDPTKRSAIVIGGGISPAVTDFIAGY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNIVTLADKD-GIWYMEILSGHQYVA----IKFPDDKYAVFPNTFYLGHVDFNDKENTI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKYSSLANTNKNVW---VLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVI 181 | :||::| : :|: | || 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMS-ATVSASANDAIQKIDPYVKNGLAESSMTSVILPSVKTAREGVALIAKIVTEKGAAE
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                                                                                                                                                                                                         ----VAAHPKPFGTKVIDEMK----GLEKTWIAEQDKSTKEISDLVVSDPKAAQEKADKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----EKSADNQN--------KQITDVSKISGLVNERKSEIMAAKADANKHFGL 78
                                                                                                                                                                                                                                           ADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDKQPDKQQESLDKL
                                                                                                                                                                                                                                                                                                                     KTKNKFFTSILKNLG--YSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDI 384
                                                                                                                                                                                                                                                                                                                                                         LDQMALDGKGKPKSKKAVKG-----YAYPISNPNVMEAHIFQLKKDIPAELGGVMWLSIG
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99 MW; B9394DC94C19AE4D CRC64,
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sekeyova Z., Roux V., Raoult D.; "Phylogenetic analysis of Rickettsia spp. by comparing to gene D coding for an intracytoplasmic protein."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rickettsia felis (Rickettsia azadi).
Bacteria; Proteobacteria; alpha subdivision;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Antigenic heat-stable 120 kDa protein (PS12
(Protein PS 120) (Fragment).
SCA4 OR D.
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GIYEGKANPEITSEKTKAV-SRGIDKSTAIPE--DKQALKDAANEAALDR
                                                                                                                                                                                                                                                                                 GITDAVIKSNLSTEDKGTMLIAVGDKVNASELSN---AEKQKLLGSVLKKGVEAQVLSPE 594
                                                                                                                                                                                                            \tt QQQLMQQNLDKITAEQTKNA----QITEVQGILANPAFNTIAKTEAIQNVTTKVLDSPIK
                                                                                                                                                                                                                                 VTDFIAGYLAGIKAWNLKNSDKKTKIT-TDKIEINLGFD------VQDTSTKERLEQIA 283
                                                                                                                                                                                                                                                                                                                    --TGRYINLTYKTEEAGWL----AGYANASFLAKKFPSDPTKRSAIVIGGGI-----SPA 231
                                                                                                                                                                                                                                                                                                                                                                                        KYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIP--- 182
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                                                                                                     VFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLAT----E
                                                                                                                                        AEIKGETLESI----TKVVAESPLNGQDK
                                                                                                                                                                         SKDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYS 343
                                                                                                                                                                                                                                                                                                                                                       -KSKMLEATVAIALNSENGE------PKQKQQMLEKAVDV-GLSLKDDASRVTAID 537
                                                                    ----ASHKTMAPTEKISTIESVEKGVAESITDL
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Search completed: July 18, 2002, 15:30:19 Job time: 66 sec

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Result
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Maximum Match 100%
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

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         /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/AB_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/Dackfiles1.pep:*
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   Gapext 0.5
4 US-08-961-083-8

US-08-396-957A-5

US-08-396-957A-4

US-08-313-412-1

US-08-313-412-1

US-08-313-42-8

US-09-336-347-36

US-09-308-347-36

US-08-923-992A-4

US-08-790-912-4

US-08-790-912-4

US-08-790-912-4

US-08-409-995-4

US-08-685-467-4

US-08-913-942-4

US-08-913-942-1

US-08-913-942-2

US-08-923-992A-2

US-08-913-942-2

US-08-685-157-2

US-08-685-157-2

US-08-913-947-2

US-08-913-947-2

US-08-685-15-32

US-08-685-15-32

US-08-685-15-32

US-08-913-942-2

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8, Appli
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107, Appli
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45	44	43	42	41	40	39	38	37	36	35	34	မ	32	31	30	29	28
106.5	106.5	106.5	107	107	107.5	108	108.5	109.5	109.5	109.5	110	110.5	110.5	110.5	111	111.5	111.5
4.6	4.6	4.6	4.7	4.7	4.7	4.7	4.7	4.8	4.8	4.8	4.8	8	4.8	<b>4</b> . 8	4.8	4.8	4.8
2432	1183	894	753	703	693	941	693	607	607	607	1579	2052	1964	1164	1128	1098	1098
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US-09-074-658-15	US-08-447-031A-2	US-08-867-941-15	US-08-646-273-36	US-08-646-273-25	US-08-235-836C-72	US-09-336-447A-9	US-08-235-836C-68	US-08-913-942-6	US-08-685-467-6	US-08-409-995-6	US-08-755-587-184	US-08-790-912-2	US-08-790-912-3	US-08-923-992A-10	US-08-923-992A-6	US-09-268-347-44	US-09-669-974-32
Sequence 15, Appl	Sequence 2, Appli	15	36	25	72	9	Sequence 68, Appl	ģ		Sequence 6, Appli	Sequence 184, App	Sequence 2, Appli	Sequence 3, Appli	Sequence 10, Appl	Sequence 6, Appli	Sequence 44, Appl	Sequence 32, Appl

ALIGNMENTS

## ; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-961-083-8 RESULT 1 US-08-961-083-8 Sequence 8, Application US/08961083 Patent No. 6159469 GENERAL INFORMATION: APPLICANT: Choi et. al. TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 328 amino acids REFERENCE/DOCKET NUMBER: PB TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504 FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: Brookes, A. Anders ZIP: 20850 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452 CORRESPONDENCE ADDRESS: PRIOR APPLICATION DATA: APPLICATION NUMBER: SOFTWARE: ASCII Text CURRENT APPLICATION DATA: COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS VETSION 6.2 SOFTWARE: ASCII Text TRENT APPLICAMENT STREET: 9410 Key West Avenue CITY: Rockville TYPE: NAME: Brookes, A. Anders REGISTRATION NUMBER: 36, CLASSIFICATION: 435 APPLICATION NUMBER: FILING DATE: COUNTRY: STATE: ADDRESSEE: 20850 amino acid Maryland USA Human Genome Sciences, US/08/961,083 36,373 PB340P2 storage

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61 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGA---LTGGEITSVD 117

Query Match Best Local S Matches 98

y Match 8.8%; Sco Local Similarity 25.7%; Pre hes 98; Conservative 56;

Score 203; DB 4; Length 328; Pred. No. 1.5e-10; Score 203; DB 4; Indels 84;

Gaps

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US-08-396-957A-5
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                 TELEFAX: (212) 751-684
TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/487,716
FILING DATE: 05-MAY-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/60
FILING DATE: 05-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                            REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 ILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 SSTAELE-----GKYSSLANTNKNVWVLSGFOHGDAFTRWLKIPENKOLFTEKNII 168
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/020,245 FILING DATE: 19-FEB-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 01-MAR CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: NEW YORK STATE: NEW YOR
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   LENGTH:
                                                                                           TELEPHONE:
                                                                                                                                                 REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                       (212) 751-6849
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                                                                                              (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLOPPY DISK
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01-MAR-1995
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US-08-396-957A-4
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; IDENTIFICATION METHOD:
; OTHER INFORMATION: p39a protein sequence
US-08-396-957A-5
                                                                                                                                                                                                                                          Sequence 4, Application US/08396957A Patent No. 5780041
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                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: SIMPSO
COMPUTER READABLE FORM:
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ORIGINAL SOURCE:
                                                                                                                            NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                TITLE OF INVENTION:
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NAME/KEY: p39a
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                                                                                                                                                                                                                                                                                                                                                                                           413 KTIPAEEVRKTLEIP 427
                                                                                                                                                                                                                                                                                                                                                        311 KVLERKIVNKEIIVP 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 TKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 AAGLAGIGVIEAAKNLGDGYYVIGADQDQS--YLAPKN-FITSVIKNIGDALYLITGE-Y 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 --LANTNKN----VWVLSGFQHGDAFTRWLKIPENKQLFTEKNII--ILGIDWTDTENVI 181
                                                        CITY: NEW YORK STATE: NEW YOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 ANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAELEGKYSS-- 129
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                                COUNTRY:
                                                                                         STREET:
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Local Similarity 26.9%;
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STRAIN: Sh-2-82
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STRANDEDNESS:
                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDLDNLKRNGSDLIW-LVGYMLTDA--SLLVSSENPKI--SYGIIDPIYGDDVQIPENLI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSKKIKISMLV---DGVLDDKSFNSSANEALLRLKKDFPENIEEVFS--CAISGVYSSYV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGPLTEI-FSDIIANQND-RYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLY 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTGRYINLTYKTEEAGWLAGY--ANASFLAKKFPSDPTKRSAIVIG--GGISPAVTD-FI 236
                     10154
                                                    NEW YORK
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                                                                                         345 PARK AVENUE
                                      USA
                                                                                                                                                                SIMPSON, WARREN; SCHWAN, TOM G. VENTION: ANTIGENIC PROTEINS AND VENTION: GENES ENCODING SAME OF
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                                                                                                              MORGAN & FINNEGAN, L.L.P
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Pred. No. 2.6e-08;
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                                                                                                                                                                  BORRELIA BURGDORFERI.
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COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS

MEDIUM TYPE:

FLOPPY DISK

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TELEX: 421792
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/487,716
FILING DATE: 05-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
PRIOR APPLICATION NIMBER: 07/664,731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
08/020,245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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189
                                                                    143
                                                                                      202 YANASFLAKKFPSDPTKRSAIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITTD 260
                                                                                                                                                                        143
                                261 KI----EINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANQ--NDRYL 314
                                                                                                                                  93 YRFSDVAKVAALQNPDMKYAI-----IDPIYSNDPIP-ANLVGMTFRAQEGAFLTG
                                                                                                                                                                                                        37
                                                                                                                                                                                                                                         87
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OTHER INFORMATION: se
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: p39'
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL TYPE:
CELL LINE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL
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YIGSFADLEAGRSVATRMYSDEID-----IIHHAAGLGGIGAIEVAKELGSGHYI 238
                                                                    YIAAKL----
                                                                                                                                                                   FQHGD-AFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAG
                                                                                                                                                                                                     GTFDDKSFNESALNGVKKVKEEFKIELVLKESSSNSYLSDLEG----LKDAGSDLIWLIG
                                                                                                                                                                                                                                       GTVNDNSFNQSSWEAIQQLGALTGGEITSVDSST----AELEGKYSSLANTNKNVWVLSG 142
                                                                                                                                                                                                                                                                       ch 7.0%; Score 162; DB 1; Length 339; Similarity 22.8%; Pred. No. 9.2e-07; 85; Conservative 69; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISOLATE:
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                                                                                                                                                                                                                                                                                                                                                                          sequence.
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                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 716-263-1600 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
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TELECOMMUNICATION INFORMATION: 716-263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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140 NS-LAIKFRNEEAAFLAGYIAAKMSRKE------KIGFLTGPMSEHLKDFKFGFK 187
                                  184 GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIG---GGISPAVTDFIAGYL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 -SNKESYEKFLKE 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 LGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDKQP 434
                                                                      92 EVQKNPLNLFWLI-GYRFSDL-----SVKLSYERPDIYYGIIDAFDYGDIQ--VPK 139
                                                                                                                                              34 VLAHGSFYDKGYNQSVHDGVVKLRDNFGIKLITKSLRPYPIEGKRLLTVDE--AMTEDAY 91
                                                                                                                                                                              83 VTAGGTVNDNSFNQSSWEAIQQLG------ALTGGEITSVDSSTAELEGKY 127
                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                      SSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGI----DWTDTENVIPT 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGVDEDQAYL---APDNVITSTTKDVGRAL----NIFT--SNHLKTNTFEGGK---LIN
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                                                                                                                                                                                                                                                                                                                                                                                                353 amino acids
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Godfrey M.D., Henry P.
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                                                                                                                                                                                                                  Score 144; DB 4; I
Pred. No. 4.4e-05;
4; Mismatches 131;
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US-09-336-447A-15
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CURRENT FILING DATE: 1999-06-21
NUMBER OF SEO ID NOS: 98
SOFTWARE: PATENTIN VET. 2.1
SEO ID NO 15
LENCTH: 889
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 110; Conserv
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APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF
FILE REFERENCE: ANCY:024
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APPLICANT: HANSEN, ERIC J.
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  615
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                                                                                                                                                      SGRLIDQKADIDNNINHIYELAQQQDQHSSDIKT-----LKKNYEEGLLELSGHLIDQ
EAIDALNKASSENTONI - - EDLAAYNELQDAYAKQQTEAIDALNKASSENTON
                                  EAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDKQPDKQQESLDKLITDINKN 451
                                                                            KADLTKDIKALESNVEEGLLDLSGRLIDQKADIAQN--QANIQDLAAYNELQDQYAQKQT
                                                                                                                KSN-SRNLAGFEFGKKSATVYLG--IKDRFVDIADTSLEGNDKKLA-----T
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                                                                                                                                                                                                                                AVNGSQLYALAAAVDDNQYDIEKNQDDIAKNQADIAKNQADIQTLENDVGKE----LLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATISGG-----RQNEASGDRSTVAGGEQNQAIGKYSTISG---GRQNE---ASGDRS-- 293
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COPE, LESLIE D.
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Sequence 8, Application US/08973462B
Patent No. 6191270
GENERAL INFORMATION:
APPLICANT: DAUBERSIES, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STATILE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER APPLICATION NUMBER: FCT/FR96/00894
EARLIER APPLICATION NUMBER: FCT/FR96/00707
EARLIER APPLICATION NUMBER: FCT/FR96/0071
EARLIER APPLICATION NUMBER: FCT/FR96/00894
US-09-308-375-2
, Sequence 2, Application US/09308375
, Patent No. 6300117
, GENERAL INFORMATION:
, APPLICANT: Genencor International,
, TITLE OF INVENTION: Proteases From
, FILE REFERENCE: GC394-PCT
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Best Local Similarity
Matches 85; Conser
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEEIKDEPVQKEVEKETVSIIEEMEENIVDVLEE---EKED-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIF---SDIIANQNDRYLIG 316
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                                                                                                                                                                                                                                    US-09-268-347-36
    APPLICANT: LOOSMOTE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE.
FILE REFERENCE: 1038-860
CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 36
FENOME: 7,111
                                                                                                                                                                          Sequence 36, Application US/09268347 Patent No. 6335182 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/308,375
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: EP9719636.4
EARLIER FILING DATE: 1997-09-15
NUMBER OF SEO ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
SEO ID NO 2
LENGTH: 2285
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LENGTH: 2411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-923-992A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08923992A Patent No. 6280738
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Best Local Similarity 20.8%;
Matches 108; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: Tai, Joseph Y.

APPLICANT: Blake, Milan S.

TITLE OF INVENTION: No. 6280738-IgA FC Binding Forms of TITLE OF INVENTION: Streptococcal Beta Antigens
                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               736
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                                                                                                                                                                                                                                                                      STREET: 1100 New CITY: Washington STATE: D.C.
                                           CLASSIFICATION:
                                                              APPLICATION NUMBER: FILING DATE: 05-SEE
                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 GLGLVFPLSAIATISAGCWDKETTKEEKSADNQNKQI-----TDVSKISG-----LVN 59
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                                             05-SEP-1997
N: 536
                                                                               US/08/923,992A
  US 60/024,707
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Pred. No. 0.1;
                                                                                                                          Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
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US-08-790-912-4
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REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 mino acids
TYPE: amino acid
                                                                                                                                                                                                                                                         Sequence 4, Application US/08790912
Patent No. 5976542
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 5.3%;
est Local Similarity 18.2%;
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                             TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT TITLE OF INVENTION: OF STREPTOCOCCUS PNEUMONIAE INFECTION NUMBER OF SEQUENCES: 10
                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
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                                        ZIP: 19103-2398
                                                     COUNTRY:
                                                                            STATE:
                                                                                              CITY: Philadelphia
                                                                                                       ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, STREET: 1601 Market Street, 36th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
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                                                                         Pennsylvania
                                                           USA
                                                                                                                                                                                                                         Plaut, Andrew G
                                                                                                                                                                                                                                          Weiser, Jeffrey N.
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Pred. No. 0.032;
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; MOLECULE TYPE:
US-08-790-912-4
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ATTORNEY/AGENT INFORMATION:
NAME: LEALY, KALLYN
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 7600-401
TELECOMMUNICATION INFORMATION:
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Best Local S
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                                                                                                                                                                                                                                                                                      1636
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1756 FKKAMYEERKNKFDSLNKVTFDDTRQPWTSYATKTISTVEELQTL 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                373 VYL---GIKDREVDIADT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 29-JAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS
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                                                                                                                                         ELLAAKGFKDGMVPYISNQYEDDAKQNGKTISIYGKTRGLVTDDLVLRKVFNGQFNNWTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDYWYRIL-----DEQGREKLYRNILVYDAYKFGDDTTVDKATVEAQ------ 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFVISTISSLGFGAYDRYRNNEHRAGAELNK------FVEDNAQETAKRQRD---H 1401
                                                                      AKKE-FEEK----
                                                                                                                                                                                                                                                                                  QKLNSFNSLIENDILSAREYKNGDVERNGYHTIKLFSPIYSALSSEKGTPGDLMGRRIAY 1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NQND-----TSILKNL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----FDSSNPAMKYFFGPVGNKVVHNKHGAYATGDSVYYMGYRMLDKDGAITYTH-- 1494
                                                                                                                                                                                                                                                                                                                                                                                                                            NMFDVIYMLEYLEGMSIVNRLSDVQKVNALRKIENKYVRDADGNDVYATNVIKNITMADA 1635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAELEGKYSSLANTNK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1861 amino acids
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Pred. No. 0.1
                                                                                                                                                                                                        ----SLEGNDKKLATEAI-----SE 403
                                                                  -----TKTIPAEEVRKTL 424
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US-09-336-447A-5

Sequence 5, Application US/09336447A Patent No. 6310190

RESULT

CORRESPONDENCE ADDRESS:

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                                                                                                                                                                                      RESULT 12
US-09-074-658-75
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CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 892
                                                                                                                                 Sequence 75, Application US/09074658 Patent No. 6184371 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.2%; Score 119; DB 4; Length 892; Rest Local Similarity 20.8%; Pred. No. 0.039;
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APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS
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APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
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APPLICANT: Run-Pan Du
APPLICANT: Quijun Wang
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES
                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                      LEIPEMPDKQPDKQQESLDKLITDI 448
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                                                                                                                                                                                                                                                                                                                                                       -ATVYLGIKDRFVDIAD----TSLEGNDKKLATEAISEAKKEFEEKTKTIPAEE--VRKT 423
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                                                                                                                                                                                                                                                         KKDAQIAKAQANENKDGIAKNQADI 599
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                                                                                                                     Loosmore,
                                                                                                                     Sheena M
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US-08-409-995-4
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Sequence 4, Application US/08409995
Patent No. 5646259
GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen I
APPLICANT: St. Geme III, Joseph
TITLE OF INVENTION: Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.1%; Score 117.5; DB Best Local Similarity 19.5%; Pred. No. 0.058; Matches 79; Conservative 68; Mismatches 1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,658
FILING DATE: 08-MAY-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 LANTNKNVWVL------SGFQHGDAFTRWLK-IPENKQLFTEKNIII-LGIDWTDTE
                                                                                                                                                                                                                                                                        337 LKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRF
                                                                                                                                                                                                                                                                                                                      541 ----ASKAVSRPEQLSHNAARISE-FSDYADDGKYKYLLGK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 A-RHENLSAQAYTGGGRILPDPMDYRSGSWLAKLGYRFGGRHYVGGVFEDTKQ---RYDI 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 KONKKAEYFLAEGESELKPAAKLAGNGNYLKNOLNRWVEERKKNNOSLSAEEEAMVREAO 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 ANKHEGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGE--ITSVDSSTAELEGKYSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 KETTKEEKSADNONKOITDVSKISG------LVNERK-----SEIMAAKAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVIP--TGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFI 236
                                                                                                                                                                                                                                                                                                                                                                   LEQIASK -- DKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSI 336
                                                                                                                                                                                                                                                                                                                                                                                                                   ACRASADKPYSYDSSDRFHYREQHNVLNALFEKSLKNKWTKHHLTLGFGYD------
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  T: Barenkamp, Stephen I.
T: St. Geme III, Joseph
INVENTION: Haemophilus
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  III, Joseph W.
Haemophilus Adhesion
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; STRANDEDNESS: dou
; TOPOLOGY: unknown
US-08-409-995-4
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Best Local S
Matches 109
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 4:
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NAME: Silva, Robin M.
REGISTRATION UNMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61053/RFT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
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LENGTH: 1912 amino acids
737 TFVKTENLTTSIDEDNPTDNGKDDALKAGDTLTFKAGKN
                                    413 KTIPAEEVRKTLEIPEMPDKQPDKQQESLDKLITDINKN 451
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Local Similarity 21.0%; Pred. No. 0.
hes 109; Conservative 65; Mismatche
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TELEFAX: (415) 398-3249
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                                                                                                                      KKSNSRNLAGFEFGKKSATVYLGIKDR-FVDIADTSLEGNDKKLATEAISEAKKEFEEKT
                                                                                                                                                                                                   ANQNDRYLI------GVDTDQSLVYTKTKNKFFTSILK--NLGYSVFSVLSDLYT 353
                                                                                                                                                                                                                                                                                       KKTKITTDKIEI-----NLGFDVQ-DTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDII 306
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                                                                               K-----GGFETVKTGAT----DADRGKVTVKDATANDADKKVAT--VKDVATAINSAA 736
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TELEFAX: (415) 398-3249
TELE; 910 277299
INFORMATION FOR SEQ ID NO: 4:
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APPLICANT: Barenkamp,
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LENGTH: 1912 amino acids
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REFERENCE/DOCKET NUMBER: A-61053-2/RFT/RMS
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                               539 TNVASGLRAYDDANF------DVLNNSATDLNRHVEDA------YKGLLNLNEKNAN 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/01 FILING DATE: 22-JUL-1996
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 GLGLVFPLSAIATISAGCWDKETTKEEKSADNQNKQI-----TDVSKISG-----LVN 59
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    KKTKITTDKIEI-----NLGFDVQ-DTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDII 306
                                                                                                                                                                                   DAFTRWLKIP-----ENKQLFTEKNIIIL-----GIDWTDTENVIPTGRYINLTYK 192
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                                                                                         TEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGIKAWNLKNSD 252
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Four Embarcadero Center, Suite 3400
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Sequence 33, Application US/09377155
Patent NO. 6197312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard Anselm APPLICANT: MOXON, E. Richard APPLICANT: MOXON, E. Richard Paul APPLICANT: MOXON, E. Richard C. CURENT: 10 NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128
CURRENT APPLICATION UNMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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; TYPE: PRT
; ORGANISM: Heemophilus influenzae
US-09-377-155-33
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Search completed: July 18, 2002, 09:14:54 Job time: 34 sec

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Microbiol. Immunol. 39:393-400(1995).
EMBL; D16674; BAA04082.1; .
InterPro; IPR003760; Bmp.
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MEDLINE=96163149; PubMed=8551970;
UShio S., Iwaki K., Taniai M., Ohta T., Fukuda
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NCBI_TaxID=2094;
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from Mycoplasma and the determination of the complete nucleotide
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NKHFGLNMAIVTAGGTVNDNSFNQSSWEAI----QQLGALTG-GEITSVDSSTAELEGKY 127
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SEQUENCE
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MEDLINE-21267165; PubMed-11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., S:
Moszer I., Dybvig K., Wroblewski H., Viari A.,
Blanchard A.;
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01-OCT-2001 (TrembLrel. 18, Last sequence update)
01-OCT-2001 (TrembLrel. 18, Last annotation updat
ABC TRANSPORTER XYLOSE-BINDING LIPOPROTEIN.
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                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                       μ.
                                                                                                                                                                             IJ
                      TS.
                                                                                                                                       MKLNK--KLFSILPVAALAIALPATF-----VSCAQNPNKTNSNLDSSKITDLLSQKE
                                                                                                                                                           VTETQKIVENKIKQASLETQK-----VVLITADGNIDDKSFNQQVYESQKTLKDFVDKAY 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANPT-NYKSVLGIPTMLINDNDAKDNEKASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRNLAGFEFGK----KSATVYLGIKDREVDIADTSLEGNDKKLATEAISEAKKEFEEKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSVVDAIKKSNKDTKYLIGVDTDQSKIFSPA-TVFFTSIEKHLGRTIYQVLTDIWLKKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIFSDII--ANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLT
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                                                                                                                                                                                                                    140;
                                                                                                                                                                                                                                                                                                                 proteome.
                                                                                                                                                                                                                    Conservative
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                                                                                KSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEI
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                                                                                                                                                                                                                                                                                                                 51096 MW;
                                                                                                                                                                                                                                    24.18;
VDSSTAELEGKYSSLANTIKNVWVLSGFQHGDAFTRWLKIPENK 159
                                                                                                                                                                                                                  ; Score 554.5; DB 1; Pred. No. 4.1e-24; 88; Mismatches 175
                                                                                                                                                                                                                                                                                                                 6724D4D820809CE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        439
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                                                                                                                                                                                                                                                      DB 16;
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                                                                                                                                                                                                                  175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pathogen
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RESULT
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                                                                                                                                                                                                                                                   Query Match 18.3
Best Local Similarity 28.4
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                       CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                     malp product of Mycoplasma ferment of bacterial lipoproteins. Infect. Immun. 67:6213-6216(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
p48 MEMBRANE LIPOPROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003760; Bmp. Pfam; PF02608; Bmp; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-M7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9X775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "P48 major surface antigen of Mycoplasma agalactiae is
                   169
                                                  108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQUENCE FROM
                                                                                    122
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                                                 NLRNKVYEPKKGQLLEAYKNAIDSGFRYIVLCGFTHQASL---VGLDENYIKKIKDNNII
                                                                                                                                                   KSEIMAAKADANKHEGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTA 121
                                                                                                                                                                                                                   KKIKWNKFLGLGLVFPLSAIATISAGCWDKETTKEEKSADNQNKQITDVSKISGL-VNER
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                 ILGIDWT---
                                                                                    ELEGK----
                                                                                                                                                                                  KKNKFYLFLGAA----PVLSVPLVAASCGDKYFKETEVDGVKTISTLAHITSRKGLKLREG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSAIVIGGGISPAVTDFIAGYLAGIKAWN--LKNSDKKTKITTDKIEINLGFDVQDTSTK
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                                                                                                                   LTVENAPKA---
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                                                                                                                                                                                                                                                                                                                                                                                    Lipoprotein.
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465 /
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                                                                                                                                                                                                                                                                                                                                       AA;
                 DTENV----
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465 P
51149 MW;
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                                                                                                                                                                                                                                                                   18.1%;
                                                                                                                   ---TFITDEGSVHDESFNQSGWEAVHKVSYELGLDKAQV-SGNK 107
                                                                              YSSLANTNKNVWVLSGFQHGDAFTRWLKIPENK-QLFTEKNII 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus/Clostridium
                                                                                                                                                                                                                                                     94;
                 ·IPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          termentans
                                                                                                                                                                                                                                                   Score 417; DB 2;
Pred. No. 3.1e-16;
04; Mismatches 180
                                                                                                                                                                                                                                                                                                                                     P48 MEMBRANE LIPOPROTEIN.
60AD5448CFE03C96 CRC64;
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465
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Best I
                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                         Rawadi G., Dyer K., Dujeancourt Submitted (NOV-1997) to the EMBI EMBL; AF036106; ARB99740.1; -. InterPro, IPR003760; Bmp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrembLrel. 06, 01-JUN-1998 (TrembLrel. 06, 01-JUN-2001 (TrembLrel. 17, MEMBRANE LIPOPROTEIN P48V.
                                                                                                                                                                                                                                                                                                                          Lipoprotein SEQUENCE
                                                                                                                                                                                                                                                                                                                                             Pfam; PF02608; Bmp;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasmataceae;
NCBI_TaxID=2115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycoplasma fermentans.
Bacteria; Firmicutes; Bacillus/Clostridium
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                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                          Match
                                                                                                                                                                                    KSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGAL/TGGEITSVDSSTA
                                                                                                                                                                                                                                GILYYNQKH--KSVKFTHTSPVKLDSGF----TAGEKMNTVINNVI;SSTPADVKYNPHV
                                              GIKAWNLKNSDKKTKIT-TDKIEINLGFDVQDTSTKERLEQIAS
                                                                                                                                             ELEGKYSSLANTNKNYWYLSGFQHGDAFTRWLKIPENKQLFTEKNIXILGIDWTDTENVI
                                                                                                                                                                      KQVVKNAEL----LKLKPYLITDEGKIDDKSFNQSAFEALKAINKQTGIEINSVEPS-S
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          LLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSIIKNLGYSVFSVLSD
                                                                             KW--FYSLQFNIKESAFTTGYAIASWLSEQ----DESKRVVASFGGGAFPGVTTFNEGFAK
                                                                                                  PTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLA
                                                                                                                          NFESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREELERNQIKIIGIDF-DIETEY
                                                                                                                                                                                                                    MKKSKKILLGL-SPIAAILPAVAVSC-----KNNDESNISFKEKDISKYTTINANG
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95;
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Best Local :
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EMBL; AF099211; AAD16395.1; -.
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01-MAY-2000 (TIEMBLIEL. 13, Last sequence update)
01-JUN-2001 (TIEMBLIEL. 17, Last annotation updat
MACROPHAGE ACTIVATING LIPOPROTEIN-404 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; Lipoprotein.
SIGNAL 1
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                                                                                      SVAGPAT--FETVRLANKGQYVIGVDSDQGMI--QDKDRILTSVLKHIKQAVYETLLDLI
                                                                                                                      AVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDL-
:|||| | : : ||: | ||
                                                                                                                                                                                    LYYNQKH--KSSKIYHTSPVKLDSGF-----TAGEKMNTVINNVLSSTPADVKYNPHVIL
                                                                                                                                                                                                                 --FYSLQFNIKESAFTTGYAIASWLSEQ---
                                                                                                                                                                                                                                                                                                               VVKNAEL-----LKLKPVLITDEGKIDDKSFNQSAFEALKAINKQTGIEINSVEPS-SNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKKSKKILLGL-SPIAAILPAVAVSCGNNDES-----NISFKEKDISKYTTNANGKQ
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LEKEEGYKPYVVKDKKADKKWSHFGTQ-----
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                                            YTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKL-ATEAI
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27.0%;
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MACROPHAGE ACTIVATING LIPOPROTEIN-404.

; D03F0F47EA2B1460 CRC64;
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Pred. No. 3.
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01-JAN-1998
01-JUN-2001
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Nagasawa S., Akedo H., Seya T.;
"A novel protein that participates in nonself
malignant cells by homologous complement.";
Nat. Med. 3:1266-1270(1997).
                                                                                                                                                                                                                      17-JUN-1997. KAGAKU GIJUTSU SH.
EMBL; D64083; BAA23530.1; -.
EMBL; AB026157; BAA77211.2; -.
InterPro; IPR003760; Bmp.
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Submitted
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MEDLINE-98022661; P
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                                                                                                                                                                                                                                                              Patent number JP1997157295-A/1,
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               M161Ag, a Mycoplasma fermentans gene product
production by human monocytes.";
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                                                                          VVKNAEL-----LKLKPVLITDEGKIDDKSFNQSAFEALKAINKQTGIEINNVEPS-SNF
                                                                                    EIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAEL 123
--FYSLQFNIKESAFTTGYAIASWLSEQ--
                  GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGI 243
                                     ESAYNSALSAGHKIWVLNGFKHQQSTKQY - - IDAHREELERNQIKIIGIDF - DIETEYKW
                                                       EGKYSSLANTNKNVWVLSGFOHGDAFTRWLKIPENKOLFTEKNIIILGIDWIDTENVIPT
                                                                                                                MKKSKKILLGL-SPIAAILPAVAVSCGNNDES-----NISFKEKDISKYTTINANGKQ
                                                                                                                                   IKWNKFLGLGLVFPLSAI-ATISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNERKS 63
                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                          Matsumoto M.;
                                                                                                                                                                                                                                                                                                                                                                                                          M., Seya T.;
(APR-1999) t
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                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                      273:12407-12414(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=9359703;
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47862 MW;
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                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Sin
Matches 128;
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"Differential posttranslational processing confers intraspecies variation of a major surface lipoprotein and a macrophage-activating lipopeptide of Mycoplasma fermentans.";
Infect. Immun. 67:760-771(1999).
EMBL; AF099210; AAD16394.1; -.
InterPro; IPR003760; Emp.
Pfam; PF02608; Emp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-INCOGNITUS;
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NCBI_TaxID=2101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma incognitus.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MACROPHAGE ACTIVATING LIPOPROTEIN-404 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                        VVKNAEL-----LKLKPVLITDEGKIDDKSFNQSAFEALKAINKQTGIEINNVEPS-SNF 106
                                                                                                                                                                                                                                                                                                                                                                MKKSKKILLGL-SPIAAILPAVAVSCGNNDES-----NISFKEKDISKYTTNANGKQ
  LYYNQKH--KSSKIYHTSPVKLDSGF
                                          KAWNLKNSDKKTKI-TTDKIEINLGEDVQDTSTKERLEQIAS------KDKPSTLL
                                                                                                                                  GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGI 243
                                                                                                                                                                                                                                                                                                     EIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAEL
                                                                                                                                                                                                                                                                                                                                                                                                           IKWNKFLGLGLVFPLSAI-ATISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNERKS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYYNQKH--KSSKIYHTSPVKLDSGF----TAGEKMNTVINNVLSSTPADVKYNPHVIL
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                                                                                         --FYSLQFNIKESAFTTGYAIASWLSEQ---DESKRVVASFGGGAFPGVTTFNEGFAKGI
                                                                                                                                                                                 ESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREELERNQIKIIGIDF-DIETEYKW
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Pred. No. 5.8e
)1; Mismatches
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MACROPHAGE ACTIVATING LIPOPROTEIN-404.
B6D09A8812AC3171 CRC64;
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-TAGEKMNTVINNVLSSTPADVKYNPHVIL
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"Differential posttranslational processing confers intraspeci-
variation of a major surface lipoprotein and a macrophage-act
lipopeptide of Mycoplasma fermentans.";
Infect. Immun. 67:760-771(1999).
EMBL; AF099212; AAD16396.1; -.
InterPro; IPR003760; Bmp.
Pfam; PF02608; Bmp; 1.
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Bacteria; Firmicutes; Bacillus/Clostridium
Mycoplasmataceae; Mycoplasma.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
MACROPHAGE ACTIVATING LIPOPROTEIN-404 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal; Lipoprotein.
SIGNAL 1
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                                                                                                                                                  LYYNOKH--KSSKIYHTSPVKLDSGF----TAGEKMNTVINNVLSISTPADVKYNPHVIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVKNAEL-----LKLKPVLITDEGKIDDKSFNQSAFEALKAINKQTGIEINNVEPS-SNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKKSKKILLGL-SPIAAILPAVAVSCGNNDES-----NISFKEKDISKYTTTNANGKQ
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                                                                                                                                                                                                   KAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQIAS------KDKPSTLL
                                                                                                                                                                                                                                                  --FYSLQFNIKESAFTTGYAIASWLSEQ---DESKRVVASFGGGAFPGVTTFNEGFAKGI
                                                                                                                                                                                                                                                                                                                                                   ESAYNSALSAGHKIWVLNGFKHQQSIKQY - - IDAHREELERNQIKI (GIDF - DIETEYKW
                                                                                                                                                                                                                                                                                                                                                                                                    EGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIII:GIDWIDTENVIPT
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429 /
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                                              FETVRLAANKGQYVIGVDSDQGMI--QDKDRILTSVLKHIKQAVYETLLDL
YTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADT:3LEGNDKKL-ATEA
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27.0%;
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Pred.
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MACROPHAGE ACTIVATING LIPOPROTEIN-404

; B6D08CF975AC3171 CRC64;
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No. 5.
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.8e-15;
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Best Local
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01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-JUN-2001 (TYEMBLREL. 17, Last annotation update)
MACROPHAGE ACTIVATING LIPOPROTEIN-404 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal; Lipoprotein.
SIGNAL 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Pfam; PF02608; Bmp; 1.
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Bactlius/Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                      VILSVAGPAT -- FETVRLANKGQYVIGVDSDQGMI -- QDKDRILTSVLKHIKQAVYETLL
                                                                                                      TLLAVAGPLIEIFSDIIANQNDRYLIGVDIDQSLVYIKTKNKFFTSILKNLGYSVFSVLS
                                                                                                                                        KGILYYNQKH--KSSKIYHTSPVKLDSGF----TAGEKMNTVINNVLSSTPADVKYNPH
                                                                                                                                                       AGIKAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQIAS-------
                                                                                                                                                                                                                                             SHESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREELERNQIKIIGIDF-DIETE
                                                                                                                                                                                                                                                                      AELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENV
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          EAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQPDKQQESLDKLITDINK
                                    DLILEKEEGYKPYVVKDKKADKKWSHFGTQ-----
                                                                                                                                                                                            YKW--FYSLQFNIKESAFTTGYAIASWLSEQ---DESKRVVASFGGGAFPGVTTFNEGFA
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428 AA;
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                                                            YTKKSNSRNLAGFEFGKKSATYYLGIKDRFYDIADTSLEGNDKKL-AT
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47960
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26.8%;
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Pred. No. 6.2e-15;
7; Mismatches 178
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MACROPHAGE ACTIVATING LIPOPROTEIN-404.

; D6B69C0BA969CFE1 CRC64;
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                                    -KEKWIGVAENHFSNTEEQAKIN
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Best Loc
Matches
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"Differential posttranslational processing confers intraspecies
variation of a major surface lipoprotein and a macrophage-activating
lipopeptide of Mycoplasma fermentans.";
Infect. Immun. 67:760-771(1999).
EMBL; AF099213; AAD16397.1; -.
InterPro; IPR003760; Bmp.
pfam; pF02608; Bmp; 1.
Signal; Lipoprotein.
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Bacteria; Firmicutes; Bacillus/Clostridium
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01-MAY-2000
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Local Similarity
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                                                                                                 KEAIKMFKE---
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                                                                                                                                                                                                                                                                               SVAGPAT -- FETVRLANKGQYVIGVDSDQGMI -- QDKDRILTSVLKHIKQAVYETLLDLI
                                                                                                                                                                                                                                                                                                                                                                            LYYNOKH -- KSSKIYHTSPVKLDSGF
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nilarity 26.8%;
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                                                                                                                                                                                                                                  YTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKL-ATEAI
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Pred. No. 1e-14;
9; Mismatches 176;
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MACROPHAGE ACTIVATING LIPOPROTEIN-404

; C7A536B409A60132 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       ----TAGEKMNTVINNVLSSTPADVKYNPHVIL
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annotation updat
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Best Local Similarity 26.6%;
Matches 125; Conservative 10
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SIGNAL 1 2
CHAIN 25 3
SEQUENCE 428 AA; 4
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Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
"Differential posttranslational processing confers intraspecies variation of a major surface lipoprotein and a macrophage-activating lipopeptide of Mycoplasma fermentans.";
Infect. Immun. 67:760-771(1999).
EMBL; AF009214; AAD15736.1; -.
EMBL; AF099214; AAD15398.1; -.
EMBL; AF099215; AAD16399.1; -.
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MEDLINE-9911554; I
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                                                  SEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQPDKQQESLDKLITDINK
                                                                                                         LEKEEGYKPYVVKDKKADKKWSHFGTQ-----
                                                                                                                                                                                                              SVAGPAT -- FETVRLANKGQYVIGVDSDQGMI--QDKDRILTSVLKHIKQAVYETLLDLI
                                                                                                                                                                                                                                                                                                                          LYYNOKH--KSSKIYHTSPVKLDSGF----TAGEKMNTVINNVLSSTPADVKYNPHVIL
                                                                                                                                                                                                                                                                                                                                                                                                                                 --FYSLQENIKESAFTTGYALASWLSEQ---DESKRVVASFGVGAFPGVTTFNEGFAKGI
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(TrEMBLrel. 13, Last seq
(TrEMBLrel. 18, Last ann
MALP-404 PRECURSOR.
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-LPEDFVKYINSDKALKDGNKIDNVSERLEAIISAINK
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Pred. No. 1.4e
)1; Mismatches
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les 175;
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Q99ZH4; Q99ZH4; 01-JUN-2001

PRELIMINARY;

PRT;

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RESULT
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AC Q9
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Q9EV91;
Q9EV91;
01-MAR-2001
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Pfam; PF00532; Peripla_BP_like;
PROSITE; PS00227; TUBULIN; UNKN
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STRAIN-SF370 / ATCC 700294 / SEROTYPE
MEDLINE-21192684; PubMed-11296296;
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01-DEC-2001 (TrEMBLrel.
PUTATIVE LIPOPROTEIN.
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InterPro; IPR003760; Bmp.
InterPro; IPR001761; Peripla_BP_like
InterPro; IPR000217; Tubulin.
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                                                                                                       KIKSGDIKVP
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                                                                                                                                                                               VLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKK
                                                                                                                                                                                                         AGVFNEAKAINEKRSEADKVWVIGVDRDQKDEGKYTSKDGKEANFVLASSIKEVGKAVQL
                                                                                                                                                                                                                                                                                     KAWNLKNSDKKTKITTDKIEINLGF-----DVQDTSTKERLEQIASKDKPSTLLAVAGPL
                                                                                                                                                                                                                                                                                                                NVASVTFADHEAAYLAGIAAAK----
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 (TrEMBLrel.
                                       PRELIMINARY;
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                                                                                                                                                                                                                                                            ---VDDTIQVKVDYAGSFGDAAKGKTIAAAQYAAGAD--VIYQAAGGTG
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19,
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16,
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Created)
Last sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 232.5;
Pred. No. 7.
                                       PRT;
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                                                                                                                                                                                                                                                                                                                ----TTKTKTVGFVGGMEGTVITRFEKGFEAGV
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7.7e-06;
hes 153;
 update)
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ai H.S., Lin
J L., White J
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RESULT
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Best Local
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Q97RH0;
Q1-OCT-2001
                       SP0845.
Streptococcus pneumon
Bacteria; Firmicutes;
                                                                      01-OCT-2001
01-DEC-2001
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Streptococcus.
NCBI_TaxID=1313;
                                                           LIPOPROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipoprotein
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                        Bacillus/Clostridium group; Streptococcaceae;
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18,
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                                                                     Created)
Last sequence update)
Last annotation update)
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Pred. No. 1.1e
66; Mismatches
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RESULT
Q9CFM9
Q9CFM9
AC Q9C
DT 01-
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Best Local Similarity
Matches 110; Conserv
                        09CEM9;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-CCT-2001 (TrEMBLrel. 18,
BASIC MEMBRANE PROTEIN A.
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Tettelin H., Nelson K.E., Paldsen I.T., Elsen J.A., Read T.D.,
Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
"Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 293:498-506(2001).
EMBL; AE007390; AAK74976.1;
TIGR; SP0845; -.
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SEQUENCE FROM N.A.
STRAIN-TIGR4;
                  BMPA.
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 Lactococcus lactis
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PROSITE; PS00227; TUBULIN; UNKNOWN_1.
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InterPro; IPR000217; Tubulin.
Pfam; PF02608; Bmp; 1.
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                                                                                                                                                                                                                                                                                                       ---IVYQVAGGTGAGVFAEAKSLNESRPENEKVWVIGVDRDQEAEGKYTSKDGKESNFVL
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 lactis) (Streptococcus lactis).
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                                                                         Created)
                                           Last sequence update)
Last annotation update
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Pred. No. 2.
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Best Local Similarity 24.3
Matches 107; Conservative
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"The complete genome sequence of the lactic acid bacter lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
EMBL; AE006374; AAK05536.1;
InterPro; IPR003766; Bmp.
Pfam; PF02608; Bmp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 350 AA;
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[1]
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                      LATEAISEAKKEFEEKTKTIPAE
                                                                KNLGYSVFSVLSDLYTKKSNSRNLAG--FEFGKKSATVYLGIKDRFVDIADTSLEGNDKK
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